```
OM of: US-09-488-265-25 to: Issued_Patents_AA:*   out_format : pfs

Date: Jul 3, 2002  2:38 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_n2p.model -DEV=xlh
 -Q=/cgn2_1/USPTO_spool/US09488265/runat_03072002_091241_4286/app_query.fasta_1.4477
 -DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai
 -GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
 -LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
 -XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
 -YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US09488265_@CGN1_1_67 -NCPU=6 -ICPU=3 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-488-265-25
Query length: 1426
Database: Issued_Patents_AA:*
Database sequences: 231628
Database length: 24425594
Search time (sec): 54.640000


score_list:
Sequence           Strd Orig    ZScore   EScore Len  ! Documentation  ..
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-1 + 2185.00 3823.39  4.0e-206  441  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-2 + 2173.00 3801.50  6.3e-205  467  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-33 + 1902.00 3323.72  2.6e-178  465  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-33 + 1902.00 3323.72  2.6e-178  465  !
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-8 + 1866.00 3260.19  8.9e-175  467  !  S
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-8 + 1866.00 3260.19  8.9e-175  467  !
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2 + 1866.00 3260.19  8.9e-175  467  !
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-151-574-32 + 1862.00 3253.13  2.2e-174  467  !
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-146-424-20 + 1862.00 3253.13  2.2e-174  467  !
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-693-709-2 + 1862.00 3253.13  2.2e-174  467  !  S
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-419-448-32 + 1862.00 3253.13  2.2e-174  467  !
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-3 + 1862.00 3253.13  2.2e-174  467  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-3 + 1862.00 3253.13  2.2e-174  467  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-233-510-32 + 1862.00 3253.13  2.2e-174  467  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-3 + 1855.00 3240.79  1.1e-173  467  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-3 + 1855.00 3240.79  1.1e-173  467  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-12 + 1841.00 3216.13  2.5e-172  466  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-12 + 1841.00 3216.13  2.5e-172  466  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-35 + 1826.00 3189.68  7.5e-171  466  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-35 + 1826.00 3189.68  7.5e-171  466  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-29 + 1813.50 3167.72  1.3e-169  463  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-29 + 1813.50 3167.72  1.3e-169  463  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-1 + 1813.00 3167.40  1.4e-169  443  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-1 + 1813.00 3167.40  1.4e-169  443  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-2 + 1808.00 3158.59  4.3e-169  443  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-2 + 1808.00 3158.59  4.3e-169  443  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-2 + 1756.00 3066.25  5.7e-164  466  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-2 + 1756.00 3066.25  5.7e-164  466  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-31 + 1719.00 3001.01  2.4e-160  466  !
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-31 + 1719.00 3001.01  2.4e-160  466  !
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-2 + 1395.00 2429.48  1.6e-128  475  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-2 + 1395.00 2429.48  1.6e-128  475  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-4 + 1346.50 2343.64  9.6e-124  487  !  S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-4 + 1346.50 2343.64  9.6e-124  487  !  S
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-30 +  846.50 1463.21  1.2e-74   443  !
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-22 +  833.50 1440.01  2.2e-73   453  !
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-24 +  831.50 1436.88  3.4e-73   439  !
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-09-221-654-2 +  831.50 1436.88  3.4e-73   439  !  S
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-989-358A-2 +  831.50 1436.88  3.4e-73   439  !
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-28 +  822.00 1420.04  3.0e-72   442  !
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-26 +  811.00 1400.65  3.6e-71   442
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-627-539G-2 +  359.00  602.93  9.1e-27   468
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-627-539G-7 +  354.50  595.61  2.4e-26   446
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-2 +  346.50  580.60  1.6e-25   479  !
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-2 +  346.50  580.60  1.6e-25   479

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-1

seq_documentation_block:
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1


alignment_scores:
            Quality: 2185.00              Length:    441
              Ratio:  5.093                Gaps:      0
 Percent Similarity:  97.279   Percent Identity: 92.744

alignment_block:
 US-09-488-265-25 x US-09-121-425-1   ..

 Align seg 1/1  to: US-09-121-425-1  from: 1  to: 441

      90 AATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGA 139
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGl 17

     140 AATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACG 189
         ||||||||||||||||||||||||||||||:::|||||||||   ||||
      17 uIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspG 34

     190 AATCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTT 239
         ||||||||||||||||||||||||      ||||||||||||||||||
      34 luSerAlaIleSerProAspValProAspAspCysArgValThrPheVal 50

     240 CAAGTTTTGTCTAGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAA 289
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 GlnValLeuSerArgHisGlyAlaArgTyrProThrSerSerLysSerLy 67

     290 GAAGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCA 339
         |   ||||||||||||||||||||||||||||||||||||||||||||||
      67 sAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAlaThrAlaPheL 84

     340 AGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 389
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      84 ysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

     390 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTT 439
         ||||||||||||||||||||:::||||||||||||||||||||||||||
     101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPh 117

     440 CTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAG 489
         ||||||||||||||||||||||||||||||||||||||||||:::||||
     117 eTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgA 134
```

```
 490 CTTCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGT 539
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 134 laSerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGly 150

 540 TTCCAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTC 589
     ||||||||||||||||||||||||||||||::::::|||||||||||||||
 151 PheGlnSerAlaLysLeuAlaAspProGlySerGlnProHisGlnAlaSe 167

 590 TCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAACAACACTT 639
     ||||||||||:::|||||||||||||||||||:::|||||||||||||||||
 167 rProValIleAspValIleIleProGluGlySerGlyTyrAsnAsnThrL 184

 640 TGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGAC 689
     ||||||||||   |||||||||||||||:::|||||||||||||||||||
 184 euAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

 690 GTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATT 739
     ||||||||||||||||||||:::|||||||||   |||||||||||||||
 201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLe 217

 740 GGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACT 789
     |||||||   ||||||||||||:::|||||||||||||||||||||   |
 217 uGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrL 234

 790 TGATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACT 839
     ||||||||||||||||||||:::|||||||||||||||||||||||||||
 234 euMetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThr 250

 840 CAATTGTCTCCATTCTGTGACTTGTTCACTCACGACGAATGGATTCAATA 889
     :::|||||||||||||||   ||||||||||||||||||||   |||||
 251 GluLeuSerProPheCysAlaLeuPheThrHisAspGluTrpArgGlnTy 267

 890 CGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACC 939
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 267 rAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnP 284

 940 CATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGA 989
     ||||||||||||||||||||||||||||:::|||||||||||||||||||
 284 roLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

 990 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGA 1039
     ||||||:::|||||||||||||||||||||||||||||||||||||||||
 301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAs 317

1040 CTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCT 1089
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 317 pSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheS 334

1090 CTCACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAAC 1139
     ||||||||||:::|||:::|||||||||||||||||||||||||||||||
 334 erHisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsn 350

1140 GGTACTAAGCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGA 1189
     ||||||   ||||||||||||||||||||||||||||||||||||||||
 351 GlyThrAlaProLeuSerThrThrSerValGluSerIleGluGluThrAs 367

1190 CGGTTACGCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTG 1239
     |||||||:::|||||||||||||||||||||:::|||||||||||||||
 367 pGlyTyrSerAlaSerTrpThrValProPheGlyAlaArgAlaTyrValG 384

1240 AAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1289
     ||||||||||||||:::|||||||||||||||||||||||||||||||||
 384 luMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

1290 AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAG 1339
     ||||||||||||||||||||||||||||||:::|||||||||||||||||
 401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyAr 417

1340 ATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTG 1389
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 417 gCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyG 434

1390 GTAACTGGGAAGAATGTTTCGCT 1412
```

```
        ||||||||   ||||||||||||
     434 lyAsnTrpAlaGluCysPheAla 441

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-2

seq_documentation_block:
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2


alignment_scores:
           Quality: 2173.00              Length:    487
             Ratio:  4.995                Gaps:      2
 Percent Similarity:  89.322   Percent Identity: 85.216

alignment_block:
 US-09-488-265-25 x US-09-121-425-2   ..

 Align seg 1/1  to: US-09-121-425-2  from: 1  to: 467

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerTh 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      17 rSerGlyThrAlaLeuGlyProArgGlyAsnSerHisSerCysAspThrV 34

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      34 alAspGlyGlyTyrGlnCysPheProGluIleSerHisLeuTrpGlyGln 50

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         |||||||||:::|||||||||   ||||||||||||||||||||||||||
      51 TyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAspVa 67

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
         ||||      ||||||||||||||||||||||||||||||||||||||||
      67 lProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyA 84

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         ||||||||||||||||||||||||||||   |||||||||
      84 laArgTyrProThrSerSerLysSerLysAlaTyrSerAla..... 97

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361

      97 ..................................................  97

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         |||||||||||||||||||||||||||||||||||||||||||||||||:
      98 .ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluA 114

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         ::|||||||||||||||||||||||||||||||||||||||||||||||||
     114 snGlnMetValAsnSerGlyIleLysPheTyrArgArgTyrLysAlaLeu 130
```

```
 462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
     ||||||||||||||||||||||:::|||||||||||||||||||||||||||
 131 AlaArgLysIleValProPheIleArgAlaSerGlySerAspArgValIl 147

 512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 147 eAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaA 164

 562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC..... 602
     ||||||||::::::|||||||||||||||||||||||:::
 164 spProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

 602 ..... 602

 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLy 197

 603 .GTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTT 651
      ||||||||||||||||||:::|||||||||||||||||||||||||||
 197 sValIleIleProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyT 214

 652 TGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAAC 701
       ||||||||||||||||:::|||||||||||||||||||||||||||||
 214 hrCysThrAlaPheGluAspSerGluLeuGlyAspAspValGluAlaAsn 230

 702 TTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTT 751
     |||||||||:::|||||||||   ||||||||||||||||||||   ||
 231 PheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAspLe 247

 752 GCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGT 801
     ||||||||||:::|||||||||||||||||||||   ||||||||||||||
 247 uProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetC 264

 802 GTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
     ||||||||:::|||||||||||||||||||||||||||:::|||||||||
 264 ysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

 852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCA 901
     ||||||   ||||||||||||||||||||   ||||||||||||||||||
 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGl 297

 902 ATCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAG 951
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 297 nSerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProA 314

 952 CTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCT 1001
     ||||||||||||||||:::|||||||||||||||||||||||:::|||
 314 laGlnGlyValGlyPheAlaAsnGluLeuIleAlaArgLeuThrArgSer 330

1002 CCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGC 1051
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 331 ProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnProAl 347

1052 TACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACA 1101
     ||||||||||||||||||||||||||||||||||||||||||||||||:
 347 aThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnS 364

1102 CTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
     ::|||:::|||||||||||||||||||||||||||||||||   |||
 364 erMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGC 1201
     ||||||||||||||||||||||||||||||||||||||||||||:::||
 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAl 397

1202 TTCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAAT 1251
     ||||||||||||||||||:::|||||||||||||||||||||||||||||
 397 aSerTrpThrValProPheGlyAlaArgAlaTyrValGluMetMetGlnC 414

1252 GTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTT 1301
     ||:::||||||||||||||||||||||||||||||||||||||||||||
 414 ysGlnAlaGluLysGluProLeuValArgValLeuValAsnAspArgVal 430

1302 GTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGA 1351
     ||||||||||||||||||:::|||||||||||||||||||||||||||||
 431 ValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArgAs 447

1352 CGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAG 1401
     ||||||||||||||||||||||||||||||||||||||||||||||   |
 447 pAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaG 464

1402 AATGTTTCGCT 1412
     ||||||||||||
 464 luCysPheAla 467
```

```
seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-33

seq_documentation_block:
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
```

```
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33


alignment_scores:
            Quality: 1902.00              Length:    467
              Ratio:  4.507                Gaps:      2
 Percent Similarity:  90.364    Percent Identity: 77.088

alignment_block:
 US-09-488-265-25 x US-08-868-435-33   ..

 Align seg 1/1  to: US-08-868-435-33  from: 1  to: 465

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||   :::::::::   |||||||||   |||   |||:::::::::
       1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
           ::::::|||   :::      |||   |||   ||||||||||||||
      17 gValSerAlaAlaProSerSerAlaGly...SerLysSerCysAspThrV 33

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         |||||   ||||||||||||   |||      ||||||||||||||||||
      33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         ||||||||||||||||||||   ||||||   ::::::|||      ::
      50 TyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLe 66

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
         :||||||   ||||||:::|||:::||||||||||||||||||||||||
      66 uProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyA 83

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         ||||||||||||||||||||||||||||||||:::   |||:::
      83 laArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
         |||||||||   |||||||||   ||||||||||||:::||||||||||
     100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLy 116

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     116 sThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluG 133

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         |||||:::|||||||||||||||||||||||||:::|||||||||||||||
     133 lnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeu 149

     462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
         ||||||:::::|||||||||:::|||||||||||||||||||||||||||
     150 AlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIl 166

     512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
         |||||||:::|||||||||||||||||||||||||:::|||||||||||||
     166 eAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaA 183

     562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
         ||||||||||||:::   ::::::|||:::|||:::|||:::|||||||||
     183 spProGlyAlaThr...AsnArgAlaAlaProAlaIleSerValIleIle 198

     612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
         |||||||:::      :::|||||||||||||||||||:::||||||
     199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLy 215

     662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
          ||||||   |||:::||||||||||:::|||   |||||||||||||||:
     215 sPheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaL 232

     712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
         ::|||||||||   ||||||||||||   |||   ||||||||||||||||
     232 euPheAlaProAspIleArgAlaArgAlaGluLysHisLeuProGlyVal 248

     762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
         :::|||||||||||||||||||||||:::||||||||||||||||   |||||
     249 ThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAs 265

     812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
         |||||||||||||||||||||||||||:::||||||||||||||||||:::|
     265 pThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnL 282

     862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
         ||||||||||||:::||||||   :::|||:::||||||||||||||||||
     282 euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

     912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
         ||||||||||||||||||||||||||||||||||||||||||||||||::
     299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl 315

     962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
         :|||||:::|||||||||||||||||||||||||:::||||||||||||
     315 eGlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnA 332

    1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
         ||||||||||||||||   ||||||   ||||||||||||||||||||
     332 spHisThrSerThrAsnSerThrLeuValSerAsnProAlaThrPhePro 348

    1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
         ||||||||||||:::|||:::|||||||||||||||||||:::||||||||
     349 LeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSe 365

    1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
         ||||||||||||||||||||||||||||||||:::|||||||||   |
     365 rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382

    1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
         ||||||||||||||   :::|||   |||||||||:::|||||||||:::
     382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

    1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
         ||||||||:::||||||||||||   |||   |||||||||::::::||
     399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGl 415

    1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
         ||||||||||||||||||:::|||:::|||||||||||||||||||||||
     415 uLysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuH 432

    1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
         ||||||||   ||||||||||||||||||||||   :::|||||||||
     432 isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448

    1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
         :::||||||||||:::|||||||||||||||||||||   |||||||||::
     449 LysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSe 465

    1412 T 1412
         :
     465 r 465

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-33

seq_documentation_block:
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
```

```
;       STREET:  340 Kingsland Street
;       CITY:  Nutley
;       STATE:  New Jersey
;       COUNTRY:  United States of America
;       ZIP:  07110
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/744,231
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/424,757
;       FILING DATE:  18-APR-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kass, Alan P
;       REGISTRATION NUMBER:  32142
;       REFERENCE/DOCKET NUMBER:  Case Docket 9339
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (201) 235-4205
;       TELEFAX:  (201) 235-2363
;   INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  465 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  104
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  119
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  205
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  228
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  337
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  374
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33


alignment_scores:
            Quality: 1902.00              Length:    467
              Ratio:  4.507                Gaps:      2
 Percent Similarity:  90.364   Percent Identity: 77.088

alignment_block:
 US-09-488-265-25 x US-08-744-231-33   ..

 Align seq 1/1  to: US-08-744-231-33  from: 1  to: 465

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||   :::::::::   |||||||||   |||   |||:::::::::
       1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
            :::::::|||   :::      |||   |||   ||||||||||||
```

```
      17 gValSerAlaAlaProSerSerAlaGly...SerLysSerCysAspThrV 33

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         |||||   ||||||||||||   |||       ||||||||||||||||||
      33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         ||||||||||||||||||||   ||||||   :::::::|||       ::
      50 TyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLe 66

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
         :||||||   ||||||:::|||:::||||||||||||||||||||||||||
      66 uProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyA 83

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         |||||||||||||||||||||||||||||||||:::   |||:::
      83 laArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
         |||||||||   |||||||||   ||||||||||||:::||||||||||||
     100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLy 116

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     116 sThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluG 133

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         |||||:::|||||||||||||||||||||||||:::|||||||||||||||
     133 lnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeu 149

     462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
         ||||||::::::|||||||||:::|||||||||||||||||||||||||||
     150 AlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIl 166

     512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
         |||||||:::|||||||||||||||||||||||||:::|||||||||||||
     166 eAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaA 183

     562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
         ||||||||||||:::   :::::::|||:::|||:::|||:::||||||||||
     183 spProGlyAlaThr...AsnArgAlaAlaProAlaIleSerValIleIle 198

     612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
         |||||||:::      :::|||||||||||||||||||:::|||||||
     199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLy 215

     662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
          ||||||   |||:::|||||||||:::|||   |||||||||||||||:
     215 sPheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaL 232

     712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
         ::|||||||||   ||||||||||||   |||   |||||||||||||||
     232 euPheAlaProAspIleArgAlaArgAlaGluLysHisLeuProGlyVal 248

     762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
         :::|||||||||||||||||||:::|||||||||||||||||   |||||
     249 ThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAs 265

     812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
         ||||||||||||||||||||||||||:::|||||||||||||||||||:::|
     265 pThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnL 282

     862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
         ||||||||||:::||||||   :::|||:::|||||||||||||||||||
     282 euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

     912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
         ||||||||||||||||||||||||||||||||||||||||||||||||::
     299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl 315

     962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
         :||||||:::|||||||||||||||||||||||||:::|||||||||||||
     315 eGlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnA 332
```

```
 1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
      ||||||||||||||||   ||||||  ||||||||||||||||||||||
  332 spHisThrSerThrAsnSerThrLeuValSerAsnProAlaThrPhePro 348

 1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
      ||||||||||||:::|||:::||||||||||||||||||:::||||||||
  349 LeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSe 365

 1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
      ||||||||||||||||||||||||||||||:::|||||||||   |
  365 rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382

 1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
      ||||||||||||   :::|||  |||||||||:::||||||||::
  382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

 1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
      |||||||||:::||||||||||||  |||  |||||||||::::::||
  399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGl 415

 1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
      ||||||||||||||||||:::|||:::||||||||||||||||||||||
  415 uLysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuH 432

 1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
      ||||||||  ||||||||||||||||||||||  :::|||||||||
  432 isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448

 1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
      :::||||||||||:::||||||||||||||||||||  |||||||||::
  449 LysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSe 465

 1412 T 1412
      :
  465 r 465
```

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-8

```
seq_documentation_block:
; Sequence 8, Application US/07923724
; Patent No. 5780292
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,724
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  1050.0240004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-923-724-8


alignment_scores:
            Quality: 1866.00              Length:    467
              Ratio:  4.453                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-07-923-724-8   ..

 Align seg 1/1  to: US-07-923-724-8  from: 1  to: 467

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
         |||||||   |||:::           |||:::   :::||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         |||||   ||||||||||||||   |||   ||||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         |||:::|||||||||||||||||:::|||||||||||||||||||||||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
         ||||   ||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         |||||||||||||:::|||||||:::|||||||||||||||||||||||
      84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
           |||||||:::|||:::|||:::|||   |||||||||||||||||||
     101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         |||||||||||||:::|||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         ||:::::|||||||||||||||||||||||||:::||||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
         :::|||:::|||:::||||||:::||||:::||||||||||:::||||||||
     151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167
```

```
 512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
     |||||||:::|||||||||||||||||||||||||||||:::||||||   |
 167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

 562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
     |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
        |||:::::::::   ||||||||||||||||   |||   ||||||::
 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
     :||||||:::|||||||||:::|||   ||||||||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

 712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
     ::|||||||||   ||||||   |||||||||      |||   ||||||
 234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
     :::||||||||||   :::|||:::   |||||||||||||||   |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
     ||||::::::   ::::::      |||:::|||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
     |||||||||||||||||||||:::|||||||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

 912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
     ||||||||||||:::|||||||||||||||||||||||||:::|||||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
     ||||::::::|||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
     ||   ||||||:::|||||||||||||||||||||||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
     ||||||:::|||||||||||||||||||||||||||||||   ::::::||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
     ||:::|||||:::|||   :::|||||||:::::::::::::||||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
     ||||||||||||:::|||   |||||||||||||||||||:::|||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
     |:::|||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
     ||||||||   :::|||   ||||||||||||   ||||||:::||||||
 434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
     :::|||||||||||||||||||||||||:::|||   ||||||   ||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

1412 T 1412
```

```
      |
     467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-8

seq_documentation_block:
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    APPLICANT:  Houston, Christine S.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,426A
;      FILING DATE:  01-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/923,724
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reed, Grant E.
;      REGISTRATION NUMBER:  P-41,264
;      REFERENCE/DOCKET NUMBER:  1050.008000I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-609-426A-8


alignment_scores:
            Quality: 1866.00                Length:    467
              Ratio:  4.453                   Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-08-609-426A-8   ..
```

```
Align seq 1/1  to: US-08-609-426A-8  from: 1  to: 467

     12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
        |||||||||   :::|||||||||   :::      |||   |||   ||
      1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

     62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
        |||||||   |||:::           |||:::   :::||||||||||
     17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

    112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
        |||||   ||||||||||||||   |||   ||||||||||||||||||
     34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

    162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
        |||:::||||||||||||||||||:::|||||||||||||||||||||||
     51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

    212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
        ||||   ||||||||||||||||||:::|||||||||||||||||||||||
     67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

    262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
        ||||||||||||||:::||||||:::|||||||||||||||||||||||
     84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

    312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
           ||||||:::|||:::|||:::|||   ||||||||||||||||||||
    101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

    362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
        ||||||||||||:::|||||||||||||||||||||||||||||||||||
    117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

    412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
        ||:::::|||||||||||||||||||||||:::||||||:::::|||||
    134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

    462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
        :::|||:::|||:::|||||||:::|||:::||||||||||:::||||||
    151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167

    512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
        |||||||:::|||||||||||||||||||||||||||:::||||||   |
    167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

    562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
        |||||   |||:::|||   |||:::|||||   |||:::|||:::|||
    184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

    612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
           |||:::::::::   ||||||||||||||   |||   ||||||::
    201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

    662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
        :||||||:::|||||||||:::|||   |||||||||||||||||||:
    217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

    712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
        ::|||||||||   ||||||   |||||||||      |||   ||||||
    234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

    762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
        :::||||||||||   :::|||:::   ||||||||||||||   |||||
    251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

    812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
        ||||::::::   ::::::      |||:::||||||||||||||||||
    267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

    862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
        |||||||||||||||||||||||:::||||||||||||||||||||||
    284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

    912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
        ||||||||||||:::|||||||||||||||||||||||||:::|||||||
    301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

    962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
        ||||:::::|||||||||||||||||||||||||||||||||||||:::|
    317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

   1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
        ||   |||||||:::|||||||||||||||||||||||||||||||||||
    334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

   1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
        ||||||:::|||||||||||||||||||||||||||||   ::::::||
    351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

   1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
        ||||:::|||||||||||||||||||||||||||||||||||||||||||
    367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

   1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
        ||:::||||||:::|||   :::|||||||||:::::::::::||||||
    384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

   1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
        ||||||||||||:::|||   |||||||||||||||||||||:::|||||
    401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

   1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
        |:::||||||||||||||||||||||||||||||||||||||||||||||
    417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

   1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
        ||||||||   :::|||   ||||||||||||   ||||||:::||||||
    434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
        :::|||||||||||||||||||||||||||:::|||   ||||||   ||
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

   1412 T 1412
        |
    467 a 467
```

```
seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2

seq_documentation_block:
; Sequence 2, Application US/08374652C
; Patent No. 5834286
;  GENERAL INFORMATION:
;    APPLICANT:  NEVALAINEN, HELENA K.M.
;    APPLICANT:  PALOHEIMO, MARJA T.
;    APPLICANT:  FAGERSTROM, RICHARD B.
;    APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;    APPLICANT:  TURUNEN, MARJA K.
;    APPLICANT:  RAMBOSEK, JOHN A.
;    APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;    APPLICANT:  HOUSTON, CHRISTINE S.
;    APPLICANT:  CANTRELL, MICHAEL A.
;    TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;    TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;    TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/374,652C
;       FILING DATE:  24-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/07058
;       FILING DATE:  27-JUL-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/925,401
;       FILING DATE:  31-JUL-1992
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  REED, GRANT E.
;       REGISTRATION NUMBER:  41,264
;       REFERENCE/DOCKET NUMBER:  1050.071001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  protein
US-08-374-652C-2


alignment_scores:
            Quality: 1866.00              Length:    467
              Ratio:  4.453                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-08-374-652C-2   ..

 Align seg 1/1  to: US-08-374-652C-2  from: 1  to: 467

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||||||||   :::|||||||||   :::     |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
         |||||||   |||:::           |||:::   :::||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         |||||   ||||||||||||||||   |||   ||||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         |||:::|||||||||||||||||:::|||||||||||||||||||||||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
         ||||   |||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         ||||||||||||||:::|||||||:::|||||||||||||||||||||||
      84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
         ||||||:::|||:::|||:::|||   ||||||||||||||||||||||
     101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         ||||||||||||||:::|||||||||||||||||||||||||||||||||

     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         ||:::::|||||||||||||||||||||||||:::|||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
         :::|||:::|||:::|||||||:::|||:::|||||||||:::||||||||
     151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167

     512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
         |||||||:::|||||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
            |||:::::::::   ||||||||||||||   |||   ||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
         :||||||:::|||||||||:::|||   |||||||||||||||||||||:
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
         ::|||||||||   ||||||   ||||||||      |||   ||||||
     234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
         :::|||||||||   :::|||:::   ||||||||||||||   |||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
         ||||::::::   ::::::      |||:::|||||||||||||||||||
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
         |||||||||||||||||||||||:::|||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

     912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
         |||||||||||||:::|||||||||||||||||||||||:::|||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
         ||||::::::|||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
         ||   ||||||:::|||||||||||||||||||||||||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

    1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
         ||||||:::|||||||||||||||||||||||||||   :::::::||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
         ||||:::|||||||||||||||||||||||||||||||||||||||||||
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
         ||:::|||||:::|||   :::|||||||:::::::::::|||||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

    1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
         ||||||||||||:::|||   |||||||||||||||||||:::|||||
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
         |:::|||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
```

```
    1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
         ||||||||  :::|||  ||||||||||||  |||||||:::||||||
     434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

    1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
         :::|||||||||||||||||||||||||||:::|||  ||||||  ||
     451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

    1412 T 1412
         |
     467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-151-574-32

seq_documentation_block:
; Sequence 32, Application US/08151574
; Patent No. 5436156
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,574
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-151-574-32


alignment_scores:
            Quality: 1862.00              Length:    467
              Ratio:  4.433                Gaps:      0
 Percent Similarity:  89.936   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-08-151-574-32   ..

 Align seg 1/1  to: US-08-151-574-32  from: 1  to: 467

  12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
     |||||||||  :::|||||||||  :::      |||  |||  ||
   1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

  62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
     |||||||  |||:::             |||:::  ||||||||||||
  17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

 112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
     |||||  ||||||||||||||  |||  ||||||||||||||||||
  34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

 162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
     |||:::|||||||||||||||||||:::|||||||:::||||||||||:::||
  51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

 212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
     ||||  |||||||||||||||||:::|||||||||||||||||||||||
  67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

 262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
     |||||||||||||:::|||||:::|||||||||||||||||||||||||
  84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

 312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
        ||||||:::||||||||:::|||  ||||||||||||||||||||
 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

 362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
     |||||||||||||:::|||||||||||||||||||||||||||||||||
 117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

 412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
     ||:::::::|||||||||||||||||||||||||:::||||||:::::|||
 134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

 462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
     :::|||:::|||||||||||||:::|||:::|||||||||:::||||||||
 151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

 512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
     |||||||::::::|||||||||||||||||||||||||:::||||||  |
 167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

 562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
     |||||  |||:::|||  |||:::||||||  |||:::|||:::|||
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
        |||:::::::::  ||||||||||||||  |||  ||||||::
 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
     :||||||:::|||||||||:::|||  ||||||||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

 712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
     ::|||:::|||  ||||||  |||||||||      |||  ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
     :::|||||||||  :::|||:::  ||||||||||||||  |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
     |||:::::::  ::::::      |||:::||||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
     |||||||||||||||||||||:::|||||||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

 912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
```

```
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
         ||||::::::|||||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
         ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

    1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
         ||||||:::|||||||||||||||||||||||||||||||   ::::::||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
         ||||:::|||||||||||||||||||||||||||||||||||||||||||
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
         ||:::||||||:::|||   :::|||||||||:::::::::::::||||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

    1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
         ||||||||||||:::|||   |||||||||||||||||||:::|||||
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
         |:::||||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

    1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
         ||||||||   ||||||   ||||||||||||   ||||||:::||||||
     434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

    1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
         :::|||||||||||||||||||||||||:::|||   ||||||||||
     451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

    1412 T 1412
         |
     467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-146-424-20

```
seq_documentation_block:
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20


alignment_scores:
            Quality: 1862.00              Length:    467
              Ratio:  4.433                Gaps:      0
 Percent Similarity:  89.936   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-08-146-424-20   ..

 Align seg 1/1  to: US-08-146-424-20  from: 1  to: 467

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||||||||   :::||||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
         |||||||   |||:::            |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         |||||   ||||||||||||||||   |||   ||||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         |||:::|||||||||||||||||:::|||||||:::||||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
         ||||   ||||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         ||||||||||||||:::||||||:::|||||||||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
         |||||||:::|||||||||:::|||   |||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         ||||||||||||||:::|||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         ||:::::|||||||||||||||||||||||||:::|||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
         :::|||:::||||||||||||:::|||:::||||||||||:::||||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
         |||||||:::::|||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
```

```
   184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

   612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
       |||::::::::::   ||||||||||||||||   |||   ||||||::
   201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

   662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
       :||||||:::||||||||||:::|||   ||||||||||||||||||||:
   217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

   712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
       ::|||:::|||   ||||||   |||||||||      |||   ||||||
   234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

   762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
       :::||||||||||   :::|||:::   ||||||||||||||||   |||||
   251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

   812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
       ||||:::::::   ::::::      |||:::||||||||||||||||||
   267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

   862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
       ||||||||||||||||||||:::||||||||||||||||||||
   284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

   912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
       ||||||||||||:::|||||||||||||||||||||||:::||||||||
   301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

   962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
       ||||::::::|||||||||||||||||||||||||||||||||||:::|
   317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

  1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
       ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
   334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

  1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
       ||||||:::|||||||||||||||||||||||||||||||   :::::::||
   351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

  1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
       ||||:::|||||||||||||||||||||||||||||||||||||||||||
   367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

  1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
       ||:::||||||:::|||   :::|||||||||:::::::::::::||||||
   384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

  1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
       ||||||||||||:::|||   |||||||||||||||||||:::|||||
   401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

  1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
       |:::||||||||||||||||||||||||||||||||||||||||||||||
   417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

  1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
       ||||||||   ||||||   ||||||||||||   ||||||:::||||||
   434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

  1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
       :::|||||||||||||||||||||||||:::|||   ||||||||||
   451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

  1412 T 1412
       |
   467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-693-709-2

seq_documentation_block:
```

```
; Sequence 2, Application US/08693709
; Patent No. 5770413
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J.J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/693,709
;      FILING DATE:  07-AUG-1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/146,424
;      FILING DATE:  02-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20011.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Signal Sequence
;      LOCATION:  1...23
;      OTHER INFORMATION:
US-08-693-709-2


alignment_scores:
            Quality: 1862.00              Length:    467
              Ratio:  4.433                Gaps:      0
 Percent Similarity:  89.936   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-08-693-709-2   ..

 Align seg 1/1  to: US-08-693-709-2  from: 1  to: 467

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||||||||   :::||||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
         |||||||   |||:::           |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
```

```
     |||||   ||||||||||||||||   |||   ||||||||||||||||||
  34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

 162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
     |||:::|||||||||||||||||||:::||||||:::||||||||:::||
  51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

 212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
     ||||   ||||||||||||||||||:::|||||||||||||||||||||
  67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

 262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
     |||||||||||||:::|||||||:::|||||||||||||||||||||||
  84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

 312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
       ||||||:::|||||||||:::|||   ||||||||||||||||||||
 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

 362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
     ||||||||||||:::|||||||||||||||||||||||||||||||||||
 117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

 412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
     ||:::::|||||||||||||||||||||||:::||||||:::::|||||
 134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

 462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
     :::|||:::|||||||||||||:::|||:::|||||||||:::||||||||
 151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

 512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
     |||||||:::::|||||||||||||||||||||||||:::||||||   |
 167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

 562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
     |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
       |||:::::::::   ||||||||||||||   |||   ||||||::
 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
     :||||||:::|||||||||:::|||   ||||||||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

 712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
     ::|||:::|||   ||||||   |||||||||      |||   ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
     :::|||||||||   :::|||:::   ||||||||||||||   |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
     ||||::::::   ::::::      |||:::||||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
     |||||||||||||||||||||:::|||||||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

 912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
     ||||||||||||:::|||||||||||||||||||||||||:::|||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
     ||||::::::|||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
     ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
```

```
 334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
     ||||||:::|||||||||||||||||||||||||||||||   ::::::||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
     ||:::||||||:::|||   :::|||||||||:::::::::::::||||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
     ||||||||||||:::|||   |||||||||||||||||||:::|||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
     |:::|||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
     ||||||||   ||||||   ||||||||||||   ||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
     :::|||||||||||||||||||||||||||||:::|||   ||||||||||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

1412 T 1412
     |
 467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-419-448-32

```
seq_documentation_block:
; Sequence 32, Application US/08419448
; Patent No. 5863533
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-419-448-32


alignment_scores:
            Quality: 1862.00              Length:    467
              Ratio:  4.433                Gaps:      0
 Percent Similarity:  89.936   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-08-419-448-32   ..

 Align seg 1/1  to: US-08-419-448-32  from: 1  to: 467

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||||||||   :::|||||||||   :::     |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
         |||||||   |||:::           |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         |||||   ||||||||||||||   |||   ||||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         |||:::||||||||||||||||||:::||||||:::|||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTG 261
         ||||   |||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         ||||||||||||||:::||||||:::|||||||||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
         ||||||:::||||||||:::|||   |||||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         ||||||||||||:::|||||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         ||:::::|||||||||||||||||||||||||:::||||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
         :::|||:::|||||||||||:::|||:::||||||||||:::||||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
         |||||||:::::|||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
         |||:::::::::   ||||||||||||||||   |||   ||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
         :||||||:::|||||||||:::|||   |||||||||||||||||||||:
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
         ::|||:::|||   ||||||   |||||||||      |||   ||||||
     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
         :::|||||||||   :::|||:::   ||||||||||||||   |||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
         ||||::::::   ::::::      |||:::|||||||||||||||||||
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
         |||||||||||||||||||||:::||||||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

     912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
         ||||||||||||:::|||||||||||||||||||||||||:::|||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
         ||||:::::|||||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
         ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

    1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
         ||||||:::|||||||||||||||||||||||||||||||   ::::::||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
         ||||:::|||||||||||||||||||||||||||||||||||||||||||
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
         ||:::|||||:::|||   :::|||||||||:::::::::::::|||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

    1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
         |||||||||||:::|||   |||||||||||||||||||||:::|||||
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
         |:::|||||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

    1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
         ||||||||   ||||||   ||||||||||||   ||||||:::||||||
     434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

    1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
         :::|||||||||||||||||||||||||||:::|||   ||||||||||
     451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

    1412 T 1412
         |
     467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-3

seq_documentation_block:
; Sequence 3, Application US/08819825
; Patent No. 5866118
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-825-3


alignment_scores:
            Quality: 1862.00              Length:    467
              Ratio:  4.433                Gaps:      0
 Percent Similarity:  89.936   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-08-819-825-3   ..

 Align seg 1/1  to: US-08-819-825-3  from: 1  to: 467

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
         |||||||   |||:::            |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         |||||   ||||||||||||||   |||   ||||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         |||:::|||||||||||||||||||:::|||||||:::|||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
         ||||   ||||||||||||||||||:::|||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         ||||||||||||||:::|||||||:::|||||||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
            ||||||:::||||||||||:::|||   ||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         ||||||||||||:::|||||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         ||:::::|||||||||||||||||||||||||||:::|||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
         :::|||:::|||||||||||||:::|||:::|||||||||:::|||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
         |||||||:::::|||||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
            |||:::::::::   ||||||||||||||||   |||   ||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
         :||||||:::|||||||||:::|||   ||||||||||||||||||||:
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
         ::|||:::|||   ||||||   |||||||||      |||   ||||||
     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
         :::|||||||||   :::|||:::   ||||||||||||||   ||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
         ||||::::::   ::::::      |||:::||||||||||||||||||||
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
         |||||||||||||||||||||||:::|||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

     912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
         ||||||||||:::|||||||||||||||||||||||||||:::|||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
         ||||::::::|||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
         ||   ||||||:::|||||||||||||||||||:::|||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

    1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
         ||||||:::|||||||||||||||||||||||||||   :::::::||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
         ||||:::|||||||||||||||||||||||||||||||||||||||||||
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
         ||:::||||||:::|||   :::|||||||||:::::::::::::||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

    1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
         ||||||||||||:::|||   |||||||||||||||||||:::||||||
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
         |:::|||||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
```

```
   1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
        ||||||||   ||||||   ||||||||||||   ||||||:::||||||
    434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
        :::|||||||||||||||||||||||||||||:::|||   ||||||||||
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

   1412 T 1412
        |
    467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-3

seq_documentation_block:
; Sequence 3, Application US/09163642
; Patent No. 6221644
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,642
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-163-642-3


alignment_scores:
            Quality: 1862.00              Length:    467
              Ratio:  4.433                Gaps:      0
 Percent Similarity:  89.936   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-09-163-642-3   ..

 Align seg 1/1  to: US-09-163-642-3  from: 1  to: 467

      12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
         |||||||   |||:::           |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
         |||||   ||||||||||||||   |||   ||||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
         |||:::|||||||||||||||||||:::|||||||:::||||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
         ||||  ||||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
         ||||||||||||||:::|||||||:::|||||||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
            ||||||:::|||||||||:::|||   |||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
         ||||||||||||:::|||||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
         ||:::::||||||||||||||||||||||||:::||||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
         :::|||:::||||||||||||:::|||:::||||||||:::||||||||
     151 ThrArgAsnIleValProPheIleArgSerGlySerSerArgValIl 167

     512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
         |||||||:::::||||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
            |||:::::::::   ||||||||||||||   |||   ||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
         :||||||:::|||||||||:::|||   ||||||||||||||||||||:
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
         ::|||:::|||   ||||||   |||||||||      |||   ||||||
     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
         :::|||||||||   :::|||:::   ||||||||||||||   |||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
         ||||::::::   ::::::      |||:::||||||||||||||||||||
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
         ||||||||||||||||||||||:::|||||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

     912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
         ||||||||||||:::|||||||||||||||||||||||||:::||||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
```

```
      317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

     1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
      334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

     1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
      351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

     1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
      367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

     1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
      384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

     1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
      401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

     1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
      417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

     1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
      434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

     1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
      451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

     1412 T 1412
          |
      467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-233-510-32

seq_documentation_block:
; Sequence 32, Application US/09233510
; Patent No. 6350602
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/233,510
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-233-510-32


alignment_scores:
            Quality: 1862.00              Length:    467
              Ratio:  4.433                Gaps:      0
 Percent Similarity:  89.936   Percent Identity: 74.518

alignment_block:
 US-09-488-265-25 x US-09-233-510-32   ..

 Align seg 1/1  to: US-09-233-510-32  from: 1  to: 467

       12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
        1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

       62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
       17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

      112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
       34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

      162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
       51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

      212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
       67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

      262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
       84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

      312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
      101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

      362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
      117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

      412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
      134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

      462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
      151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

      512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
      167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

      562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
```

```
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
     |||:::::::::   ||||||||||||||||   |||   ||||||::
 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
     :||||||:::|||||||||:::|||   ||||||||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

 712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
     ::|||:::|||   ||||||   |||||||||      |||   ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
     :::|||||||||   :::|||:::   ||||||||||||||   |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
     ||||::::::   ::::::      |||:::||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
     ||||||||||||||||||||||:::||||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

 912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
     ||||||||||||:::|||||||||||||||||||||||:::|||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
     ||||::::::|||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
     ||   ||||||:::|||||||||||||||||:::|||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
     ||||||:::|||||||||||||||||||||||||||   ::::::||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
     ||||:::|||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
     ||:::||||||:::|||   :::|||||||||:::::::::::||||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
     ||||||||||||:::|||   |||||||||||||||||||:::||||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
     |:::||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
     ||||||||   ||||||   ||||||||||||   ||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
     :::||||||||||||||||||||||||||:::|||   ||||||||||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

1412 T 1412
     |
  467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-3

seq_documentation_block:
```

```
; Sequence 3, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
;  APPLICANT: KONDO, Hidemasa
;  APPLICANT: ANAZAWA, Hideharu
;  APPLICANT: KANEKO, Syunichi
;  APPLICANT: NAGASHIMA, Tadashi
;  APPLICANT: TANGE, Tatsuya
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 81356/124
;  CURRENT APPLICATION NUMBER: US/09/155,855
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
;  EARLIER FILING DATE: 1997-04-04
;  EARLIER APPLICATION NUMBER: JP 084314
;  EARLIER FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-155-855-3


alignment_scores:
            Quality: 1855.00              Length:    467
              Ratio:  4.396                Gaps:      0
 Percent Similarity:  90.364   Percent Identity: 73.448

alignment_block:
 US-09-488-265-25 x US-09-155-855-3   ..

 Align seg 1/1  to: US-09-155-855-3  from: 1  to: 467

   12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
      |||||||||   :::|||||||||   :::      |||   |||   ||
    1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

   62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
      |||||||  ||||::            |||:::   ::::||||||||||
   17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

  112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
      |||||   ||||||||||||||   |||   ||||||||||||||||||
   34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

  162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
      |||:::||||||||||||||||||:::::||||||||||||||||||||
   51 TyrAlaProPhePheSerLeuAlaAsnLysSerAlaIleSerProAspVa 67

  212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
      ||||   ||||||:::||||||||:::||||||||||||||||||||||
   67 lProAlaGlyCysHisValThrPheAlaGlnValLeuSerArgHisGlyA 84

  262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
      ||||||||||||||:::||||||:::||||||||||||||||||||||||
   84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

  312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
          ||||||:::|||||||||:::|||:::||||||||||||||||||||
  101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLy 117

  362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
      ||||||||||||:::|||||||||||||||||||||||||||||||||
  117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

  412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
      ||::::::||||||||||:::|||||||||:::||||||::::::|||
  134 lnGluLeuValAsnSerGlyValLysPheTyrGlnArgTyrGluSerLeu 150

  462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
      :::|||:::||||||||||||:::|||:::||||||||||:::||||||||
```

```
 151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

 512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
     |||||||::::::|||||||||||||||||||||||||:::|||||| |
 167 eAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

 562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
     |||||  |||:::|||  |||:::|||||||  |||:::|||:::|||
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
        |||::::::      |||||||||||||||  |||  ||||||::
 201 SerGluAlaSerThrSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
     :|||||||:::|||||||||:::|||||::::|||||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaT 234

 712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
     ::|||:::|||  ||||||  |||||||||      |||  ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
     :::|||||||||  :::|||:::  ||||||||||||||  |||||
 251 SerLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
     ||||::::::  ::::::      |||:::||||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
     ||||||||||||:::|||||||||:::|||||||||||||||||||||:::
 284 euPheThrHisGluGluTrpIleAsnTyrAspTyrLeuGlnSerLeuAsn 300

 912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
     ||||||||||||:::|||||||||||||||||||||||||:::||||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
     ||||::::::|||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
     ||   ||||||:::|||||||||||||||||||||||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
     ||||||:::|||||||||||||||||||||||||||||||  ::::::||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
     ||||:::|||||||||||||||||||||||||||||||||||||||:::|
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerSerT 384

1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
     ||::::::|||:::|||  :::|||||||||:::::::::::::||||||
 384 hrThrAlaGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
     ||||||||||||:::|||  |||||||||||||||||||||:::::::||
 401 ValProPheAlaSerArgMetTyrValGluMetMetGlnCysGlnSerGl 417

1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
     |:::|||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
     ||||||||  ||||||  ||||||||||||  ||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1411
     :::|||||||||||||||||||||||||:::|||  ||||||||||
 451 LysGlyLeuSerPheAlaArgSerGlyGlyAspTrpGlyGluCysPheAl 467
```

```
1412 T 1412
     |
 467 a 467
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 3, 2002, 09:30:41 ; Search time 39.56 Seconds
(without alignments)
288.341 Million cell updates/sec

Title: US-09-488-265-26
Perfect score: 2470
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWEECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2185	88.5	441	4	US-09-121-425-1	Sequence 1, Appli
2	2173	88.0	467	4	US-09-121-425-2	Sequence 2, Appli
3	1902	77.0	465	4	US-08-868-435-33	Sequence 33, Appl
4	1902	77.0	465	4	US-08-744-231-33	Sequence 33, Appl
5	1866	75.5	467	1	US-07-923-724-8	Sequence 8, Appli
6	1866	75.5	467	2	US-08-609-426A-8	Sequence 8, Appli
7	1866	75.5	467	2	US-08-374-652C-2	Sequence 2, Appli
8	1862	75.4	467	1	US-08-151-574-32	Sequence 32, Appl
9	1862	75.4	467	1	US-08-146-424-20	Sequence 20, Appl
10	1862	75.4	467	1	US-08-693-709-2	Sequence 2, Appli
11	1862	75.4	467	2	US-08-419-448-32	Sequence 32, Appl
12	1862	75.4	467	2	US-08-819-825-3	Sequence 3, Appli
13	1862	75.4	467	4	US-09-163-642-3	Sequence 3, Appli
14	1862	75.4	467	4	US-09-233-510-32	Sequence 32, Appl
15	1855	75.1	467	4	US-09-155-855-3	Sequence 3, Appli
16	1855	75.1	467	4	US-09-543-744-3	Sequence 3, Appli
17	1841	74.5	466	4	US-08-868-435-12	Sequence 12, Appl
18	1841	74.5	466	4	US-08-744-231-12	Sequence 12, Appl
19	1826	73.9	466	4	US-08-868-435-35	Sequence 35, Appl
20	1826	73.9	466	4	US-08-744-231-35	Sequence 35, Appl
21	1813.5	73.4	463	4	US-08-868-435-29	Sequence 29, Appl
22	1813.5	73.4	463	4	US-08-744-231-29	Sequence 29, Appl
23	1813	73.4	443	4	US-09-155-855-1	Sequence 1, Appli
24	1813	73.4	443	4	US-09-543-744-1	Sequence 1, Appli
25	1808	73.2	443	4	US-09-155-855-2	Sequence 2, Appli
26	1808	73.2	443	4	US-09-543-744-2	Sequence 2, Appli
27	1756	71.1	466	4	US-08-868-435-2	Sequence 2, Appli
28	1756	71.1	466	4	US-08-744-231-2	Sequence 2, Appli
29	1719	69.6	466	4	US-08-868-435-31	Sequence 31, Appl
30	1719	69.6	466	4	US-08-744-231-31	Sequence 31, Appl
31	1395	56.5	475	2	US-08-819-825-2	Sequence 2, Appli
32	1395	56.5	475	4	US-09-163-642-2	Sequence 2, Appli
33	1346.5	54.5	487	4	US-08-868-435-4	Sequence 4, Appli
34	1346.5	54.5	487	4	US-08-744-231-4	Sequence 4, Appli
35	846.5	34.3	443	3	US-08-993-359-30	Sequence 30, Appl
36	833.5	33.7	453	3	US-08-993-359-22	Sequence 22, Appl
37	831.5	33.7	439	3	US-08-993-359-24	Sequence 24, Appl
38	831.5	33.7	439	3	US-09-221-654-2	Sequence 2, Appli
39	831.5	33.7	439	3	US-08-989-358A-2	Sequence 2, Appli
40	822	33.3	442	3	US-08-993-359-28	Sequence 28, Appl
41	811	32.8	442	3	US-08-993-359-26	Sequence 26, Appl
42	359	14.5	468	1	US-07-627-539G-2	Sequence 2, Appli
43	354.5	14.4	446	1	US-07-627-539G-7	Sequence 7, Appli
44	346.5	14.0	479	1	US-07-923-724-2	Sequence 2, Appli
45	346.5	14.0	479	2	US-08-609-426A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

Query Match 88.5%; Score 2185; DB 4; Length 441;
Best Local Similarity 92.7%; Pred. No. 4.3e-222;
Matches 409; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

```
Qy      27 NSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 86
           ||||||||||||||||||||||||||||:||| |||||||||| ||||||||||||||||
Db       1 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 60

Qy      87 PTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
           ||||||| |||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      61 PTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

Qy     147 YKALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY 206
           |||||||||||:|||||||||||||||||||||||||||||: ||||||||:||||||:||
Db     121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy     207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
           ||||||| ||||:|||||||||||:||| ||||||| |||| |||||||| |||||||
Db     181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

Qy     267 DTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
           :|||||||||:||||| ||||||| ||||||||||||||||||||||||||||| ||||||
Db     241 ETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300

Qy     327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
           || ||||||||||||||||||||||||||||||:|:|||||||||||| |||||||
```

```
Db    301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy    387 ESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
          |||||||||:|||||||  ||||||||||:||||||||||||||||||||  |||||||||
Db    361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy    447 DDFVEGLSFARSGGNWEECFA 467
          |||||||||||||||| ||||
Db    421 DDFVEGLSFARSGGNWAECFA 441


RESULT   2
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2


  Query Match            88.0%;  Score 2173;  DB 4;  Length 467;
  Best Local Similarity  85.2%;  Pred. No. 8.6e-221;
  Matches  415;  Conservative   13;  Mismatches   19;  Indels   40;  Gaps    2;

Qy      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:||| ||
Db      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy     61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
          ||||||||  |||||||||||||||||||||||| |||                   |||
Db     61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSA-------------------TYN 100

Qy    121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
          |||||||||||||  ||||||||||||||||||||||||:||||||||||||||||||||
Db    101 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160

Qy    181 KLADPGANPHQASPVIN-------------------VIIPEGAGYNNTLDHGLCTAFEE 220
          ||||||: ||||||||:                   ||||||:|||||||| |||||:
Db    161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy    221 SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSP 280
          |||||||||||||:||| ||||||| |||| ||||||| |||||||:|||||||||:|||
Db    221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

Qy    281 FCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNH 340
          || ||||||| |||||||||||||||||||||||||| |||||||| ||||||||||||
Db    281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy    341 TLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWT 400
          |||||||||||||||||||||:|:|||||||||||| ||||||||||||||||:||||
Db    341 TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

Qy    401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGG 460
          ||| ||||||||||:|||||||||||||||||||| ||||||||||||||||||||||||
Db    401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460

Qy    461 NWEECFA 467
          || ||||
Db    461 NWAECFA 467


RESULT   3
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33


  Query Match            77.0%;  Score 1902;  DB 4;  Length 465;
  Best Local Similarity  77.1%;  Pred. No. 3.6e-192;
```

```
  Matches  360;  Conservative   37;  Mismatches   68;  Indels    2;  Gaps    2;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |     ||| | |        |    | | |||||| |||| |  ||||||||||||| ||
Db       1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
            ::|  :|| ||:| ||||||||||||||||||  |: ||| ||| |||:|||||||
Db      60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |||||||||||||||:||||||||:||||||| :|||:|||||||||| |||||||| |
Db     120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           |||||||  ::|:| |:|||||   :|||||||:|| || |:|||:| |||||:||| ||
Db     180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           || | ||||| ||||||||:||||| |||||||||||:|||||| ||||:|| :|:||||||
Db     239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           |||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db     299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           |||:|||||||||||||:||| ||||| :| |||:||| ||| |||| | |||::||||
Db     359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           ||| |:|||||||||| |||||||| :|||:|||:|||||| |||:
Db     419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT   4
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33


  Query Match             77.0%;  Score 1902;  DB 4;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 3.6e-192;
  Matches  360;  Conservative   37;  Mismatches   68;  Indels    2;  Gaps    2;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |     ||| | |        |    | | |||||| |||| |  ||||||||||||| ||
Db       1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
            ::|  :|| ||:| ||||||||||||||||||  |: ||| ||| |||:|||||||
Db      60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |||||||||||||||:||||||||:||||||| :|||:|||||||||| |||||||| |
Db     120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           |||||||  ::|:| |:|||||   :|||||||:|| || |:|||:| |||||:||| ||
Db     180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           || | ||||| ||||||||:||||| |||||||||||:|||||| ||||:|| :|:||||||
Db     239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           |||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db     299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           |||:|||||||||||||:||| ||||| :| |||:||| ||| |||| | |||::||||
Db     359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           ||| |:|||||||||| |||||||| :|||:|||:|||||| |||:
Db     419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT   5
US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
```

```
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,724
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  1050.0240004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-923-724-8


  Query Match             75.5%;  Score 1866;  DB 1;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 2.3e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | |||||||:||||||:|
Db       1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           |||||||| |||||| |||||||||||| || |||||||| ||:| | | ||||||||||
Db      61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||::|||||||:||::| | |:||:|:||| ||||| |||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| ||| ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
```

```
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||::::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| :| |||| || || |||||||||:| || |
Db     421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT   6
US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    APPLICANT:  Houston, Christine S.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,426A
;      FILING DATE:  01-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/923,724
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reed, Grant E.
;      REGISTRATION NUMBER:  P-41,264
;      REFERENCE/DOCKET NUMBER:  1050.008000I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-609-426A-8


  Query Match           75.5%;  Score 1866;  DB 2;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 2.3e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | |||||||:||||||:|
Db       1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           |||||||| |||||| |||||||||||| || |||||||| ||:| | | ||||||||||
Db      61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::|||||||:||::| | |:||:|:||| ||||| |||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| ||| ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||| |||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||::::|||||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| :| |||| || || ||||||||||:| || |
Db     421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT   7
US-08-374-652C-2
; Sequence 2, Application US/08374652C
; Patent No. 5834286
;  GENERAL INFORMATION:
;    APPLICANT:  NEVALAINEN, HELENA K.M.
;    APPLICANT:  PALOHEIMO, MARJA T.
;    APPLICANT:  FAGERSTROM, RICHARD B.
;    APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;    APPLICANT:  TURUNEN, MARJA K.
;    APPLICANT:  RAMBOSEK, JOHN A.
;    APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;    APPLICANT:  HOUSTON, CHRISTINE S.
;    APPLICANT:  CANTRELL, MICHAEL A.
;    TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;    TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;    TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,652C
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07058
;      FILING DATE:  27-JUL-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/925,401
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REED, GRANT E.
;      REGISTRATION NUMBER:  41,264
;      REFERENCE/DOCKET NUMBER:  1050.071001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-374-652C-2


  Query Match           75.5%;  Score 1866;  DB 2;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 2.3e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | |||||||:||||||:|
Db       1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           |||||||| |||||| |||||||||||| || |||||||| ||:| | | ||||||||||
Db      61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::|||||||:||::| | |:||:|:||| ||||| |||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| ||| ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||| |||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||::::|||||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| :| |||| || || ||||||||||:| || |
Db     421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT   8
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
```

```
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,574
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-151-574-32


  Query Match             75.4%;  Score 1862;  DB 1;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 6.1e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | |||||||:|||||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| || |||||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::|||||||||:||::| | ||||:|:||| ||||| :||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
            |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||::::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || |||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  9
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20


  Query Match             75.4%;  Score 1862;  DB 1;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 6.1e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | |||||||:|||||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| || |||||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::|||||||||:||::| | ||||:|:||| ||||| :||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
            |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
```

```
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||| |||||||||||| | ||:||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| ||||||||||||||:||:| :|||::::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||| || |||| || || ||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 10
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J.J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/693,709
;      FILING DATE:  07-AUG-1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/146,424
;      FILING DATE:  02-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20011.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Signal Sequence
;      LOCATION:  1...23
;      OTHER INFORMATION:
US-08-693-709-2


  Query Match             75.4%;  Score 1862;  DB 1;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 6.1e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | |||||||:||||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| || |||||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||::|||||||:||::| | ||||:|:||| ||||| :|||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||| |||||||||||| | ||:||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| ||||||||||||||:||:| :|||::::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||| || |||| || || ||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 11
US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-419-448-32


  Query Match             75.4%;  Score 1862;  DB 2;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 6.1e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | |||||||:||||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| || |||||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||||::|||||||:||::| | ||||:|:||| ||||| :||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||:::::||||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || |||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  12
US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-825-3


  Query Match             75.4%;  Score 1862;  DB 2;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 6.1e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | |||||||:||||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| || |||||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||||::|||||||:||::| | ||||:|:||| ||||| :||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||:::::||||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || |||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  13
US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
```

```
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/163,642
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/819,825
;       FILING DATE:  18-MAR-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lambiris, Elias J.
;       REGISTRATION NUMBER:  33,728
;       REFERENCE/DOCKET NUMBER:  4758.200-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212 867 0123
;       TELEFAX:  212 867 0298
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-163-642-3


  Query Match             75.4%;  Score 1862;  DB 4;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 6.1e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | |||||||:|||||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| || |||||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||::|||||||:||::| | ||||:|:||| ||||| :|||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||::::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || |||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  14
US-09-233-510-32
; Sequence 32, Application US/09233510
; Patent No. 6350602
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/233,510
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-233-510-32


  Query Match             75.4%;  Score 1862;  DB 4;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 6.1e-188;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | |||||||:|||||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| || |||||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||::|||||||:||::| | ||||:|:||| ||||| :|||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||::::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || |||||||||:| ||||
```

```
Db    421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 15
US-09-155-855-3
; Sequence 3, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
;  APPLICANT: KONDO, Hidemasa
;  APPLICANT: ANAZAWA, Hideharu
;  APPLICANT: KANEKO, Syunichi
;  APPLICANT: NAGASHIMA, Tadashi
;  APPLICANT: TANGE, Tatsuya
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 81356/124
;  CURRENT APPLICATION NUMBER: US/09/155,855
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
;  EARLIER FILING DATE: 1997-04-04
;  EARLIER APPLICATION NUMBER: JP 084314
;  EARLIER FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-155-855-3


  Query Match             75.1%;  Score 1855;  DB 4;  Length 467;
  Best Local Similarity   73.4%;  Pred. No. 3.3e-187;
  Matches  343;  Conservative   51;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | |||||||:|||||::
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANK 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
           |||||||| || ||| |||||||||||| || |||||||| ||:||| |:||||||||||
Db      61 SAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFEGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||::||||:|||:||::| | ||||:|:||| |||||  ||||||||
Db     121 YSLGADDLTPFGEQELVNSGVKFYQRYESLTRNIVPFIRSSGSSRVIASGNKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| ||:|||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASTSNNTLDPGTCTVFEDSELADDIEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
            |||  | ||:||| :|  ||||| |||:: ::  |:||||||||||:||| |||||||
Db     241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHEEWINYDYLQSLN 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||| |||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||:|: |:| :|||:::::||||||:| |||||||::|:||
Db     361 HDNGIISILFALGLYNGTKPLSSTTAENITQTDGFSSAWTVPFASRMYVEMMQCQSEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || ||:||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVKGLSFARSGGDWGECFA 467


Search completed: July  3, 2002, 09:33:12
Job time: 151 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 3, 2002, 09:33:12 ; Search time 39.56 Seconds
(without alignments)
269.818 Million cell updates/sec

Title: US-09-488-265-27
Perfect score: 2321
Sequence: 1 NSHSCDTVDGYQCPEISHLW.....DFVEGLSFARSGGNWAECFA 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2020	87.0	441	4	US-09-121-425-1	Sequence 1, Appli
2	1902	81.9	467	4	US-09-121-425-2	Sequence 2, Appli
3	1762.5	75.9	465	4	US-08-868-435-33	Sequence 33, Appl
4	1762.5	75.9	465	4	US-08-744-231-33	Sequence 33, Appl
5	1688	72.7	466	4	US-08-868-435-12	Sequence 12, Appl
6	1688	72.7	466	4	US-08-744-231-12	Sequence 12, Appl
7	1688	72.7	467	1	US-07-923-724-8	Sequence 8, Appli
8	1688	72.7	467	2	US-08-609-426A-8	Sequence 8, Appli
9	1688	72.7	467	2	US-08-374-652C-2	Sequence 2, Appli
10	1684	72.6	467	1	US-08-151-574-32	Sequence 32, Appl
11	1684	72.6	467	1	US-08-146-424-20	Sequence 20, Appl
12	1684	72.6	467	1	US-08-693-709-2	Sequence 2, Appli
13	1684	72.6	467	2	US-08-419-448-32	Sequence 32, Appl
14	1684	72.6	467	2	US-08-819-825-3	Sequence 3, Appli
15	1684	72.6	467	4	US-09-163-642-3	Sequence 3, Appli
16	1684	72.6	467	4	US-09-233-510-32	Sequence 32, Appl
17	1676.5	72.2	463	4	US-08-868-435-29	Sequence 29, Appl
18	1676.5	72.2	463	4	US-08-744-231-29	Sequence 29, Appl
19	1672	72.0	443	4	US-09-155-855-1	Sequence 1, Appli
20	1672	72.0	443	4	US-09-543-744-1	Sequence 1, Appli
21	1672	72.0	467	4	US-09-155-855-3	Sequence 3, Appli
22	1672	72.0	467	4	US-09-543-744-3	Sequence 3, Appli
23	1667	71.8	443	4	US-09-155-855-2	Sequence 2, Appli
24	1667	71.8	443	4	US-09-543-744-2	Sequence 2, Appli
25	1596.5	68.8	466	4	US-08-868-435-31	Sequence 31, Appl
26	1596.5	68.8	466	4	US-08-744-231-31	Sequence 31, Appl
27	1588	68.4	466	4	US-08-868-435-35	Sequence 35, Appl
28	1588	68.4	466	4	US-08-744-231-35	Sequence 35, Appl
29	1562.5	67.3	466	4	US-08-868-435-2	Sequence 2, Appli
30	1562.5	67.3	466	4	US-08-744-231-2	Sequence 2, Appli
31	1322	57.0	475	2	US-08-819-825-2	Sequence 2, Appli
32	1322	57.0	475	4	US-09-163-642-2	Sequence 2, Appli
33	1275.5	55.0	487	4	US-08-868-435-4	Sequence 4, Appli
34	1275.5	55.0	487	4	US-08-744-231-4	Sequence 4, Appli
35	837.5	36.1	443	3	US-08-993-359-30	Sequence 30, Appl
36	812.5	35.0	453	3	US-08-993-359-22	Sequence 22, Appl
37	804.5	34.7	439	3	US-08-993-359-24	Sequence 24, Appl
38	804.5	34.7	439	3	US-09-221-654-2	Sequence 2, Appli
39	804.5	34.7	439	3	US-08-989-358A-2	Sequence 2, Appli
40	793	34.2	442	3	US-08-993-359-28	Sequence 28, Appl
41	791.5	34.1	442	3	US-08-993-359-26	Sequence 26, Appl
42	343.5	14.8	446	1	US-07-627-539G-7	Sequence 7, Appli
43	343.5	14.8	468	1	US-07-627-539G-2	Sequence 2, Appli
44	307.5	13.2	479	1	US-07-923-724-2	Sequence 2, Appli
45	307.5	13.2	479	2	US-08-609-426A-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT   1
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1


  Query Match             87.0%;  Score 2020;  DB 4;  Length 441;
  Best Local Similarity   89.3%;  Pred. No. 7.8e-208;
  Matches  400;  Conservative   10;  Mismatches   20;  Indels   18;  Gaps   10;

Qy       1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
           ||||||||| |||| ||||||||||||:||| ||||||||||  ||||||||||||||||
Db       1 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 60

Qy      59 PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
           ||||||| |||||| |||||| ||||||||||||||||||||||||||||||||||||||||
Db      61 PTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

Qy     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
           |||||| ||||:|||||||||||||||||||||||||||    |||||||:|||||||||
Db     121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy     175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
           ||||||| ||||||| |||| ||||||:||| ||||||| |||| ||||||| ||||||||
Db     181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

Qy     234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
           :|||||||||:||||| ||| ||| |||||||| ||||||||||||||||||| |||||||
Db     241 ETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300

Qy     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
           || |||||||||||||||||||||||||||||||:|:|||||||||||| |||||||
```

```
Db    301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy    351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
          ||| ||||||:||||||| ||||||||||:|       ||||||||||||||||||||| ||
Db    361 ESIEETDGYSASWTVPFGARAYVEMMQCQA-------EKEPLVRVLVNDRVVPLHGCAVD 413

Qy    410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
          |||||| ||||||||||||||||||||||
Db    414 KLGRCKRDDFVEGLSFARSGGNWAECFA 441


RESULT   2
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2


  Query Match             81.9%;  Score 1902;  DB 4;  Length 467;
  Best Local Similarity   81.8%;  Pred. No. 3.8e-195;
  Matches  382;  Conservative   10;  Mismatches   19;  Indels   56;  Gaps   11;

Qy      1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
          |||||||| |||| ||||||||||:||| |||||||||  ||||||||||||||||
Db     27 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 86

Qy     59 PTSSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
          ||||||| |||                 ||||||||||||||||||||||||||||||
Db     87 PTSSKSKAYSA------------------TYNYTLGADDLTPFGENQMVNSGIKFYRRY 127

Qy    119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVIN---------- 165
          ||||| ||||:|||||||||||||||||||||||    |||||||:
Db    128 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDLIEAIQKNAT 187

Qy    166 ----------VIIPEGSGYNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-L 214
                     |||||||||||||||| ||||||| |||| ||||||:||| ||||||| |
Db    188 AFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADL 247

Qy    215 PGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGA 272
          ||| ||||||| ||||||:|||||||||:||||| ||| ||| |||||||| ||||||| 
Db    248 PGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGA 307

Qy    273 GNPLGPAQGVGF-NELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVS 331
          |||||||||||| |||||||| ||||||||||||||||||||||||||||||||||:|:|
Db    308 GNPLGPAQGVGFANELIARLTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMIS 367

Qy    332 IFFALGLYNGTKPLSTTSVESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEP 390
          |||||||||||| |||||||||| |||||:||||||| ||||||||||:|       ||||
Db    368 IFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQA-------EKEP 420

Qy    391 LVRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 437
          |||||||||||||| |||||||| ||||||||||||||||||||||||
Db    421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467


RESULT   3
```

```
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33


  Query Match             75.9%;  Score 1762.5;  DB 4;  Length 465;
  Best Local Similarity   77.4%;  Pred. No. 3.4e-180;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy      2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
            | |||||| |||| |  |||||||||||||| || ::|  :|| ||:| ||||||||||||
```

```
Db      27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy      60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
           ||||||||  |:  || ||| ||||:||||||||||||||||||||| |:||||||||:||
Db      87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy     119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
           |||||::|||:|||||||||| |||||||| ||||||   ::|:| |:|||||   :||
Db     147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy     177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
           ||||||:|| || | |||:  |||||:||| |||| |  |||| |||||||:||||| |||
Db     207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy     236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
           |||||||:|||||| ||| :|| :|:||||| |||||||||||||||:|| ||||||||
Db     267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy     293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
           |||||||||| || ||||||||||:| ||||||:||||||||||||:||| |||||
Db     327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy     353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
             | |||:||| ||| |||| | |||::       ||||||| |:||||||||| ||||
Db     387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy     412 GRCKLDDFVEGLSFARSGGNWAECFA 437
           |||||:|||:|||:||||||| |||:
Db     440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT   4
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33


  Query Match           75.9%;  Score 1762.5;  DB 4;  Length 465;
  Best Local Similarity  77.4%;  Pred. No. 3.4e-180;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy       2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
           | |||||| |||| |  ||||||||||||| || ::|  :|| ||:| ||||||||||||
Db      27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy      60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
           ||||||||  |:  || ||| |||||:|||||||||||||||||||| |:||||||||:||
Db      87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy     119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
           |||||::|||:|||||||||| |||||||| ||||||   ::|:| |:|||||   :||
Db     147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy     177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
           ||||||:|| || | |||:  |||||:||| |||| |  |||| |||||||:||||| |||
Db     207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy     236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
           |||||||:|||||| ||| :|| :|:||||| |||||||||||||||:|| ||||||||
Db     267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy     293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
           |||||||||| || ||||||||||:| ||||||:||||||||||||:||| |||||
Db     327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy     353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
             | |||:||| ||| |||| | |||::       ||||||| |:||||||||| ||||
Db     387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy     412 GRCKLDDFVEGLSFARSGGNWAECFA 437
           |||||:|||:|||:||||||| |||:
Db     440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT   5
US-08-868-435-12
; Sequence 12, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-868-435-12


  Query Match             72.7%;  Score 1688;  DB 4;  Length 466;
  Best Local Similarity   74.3%;  Pred. No. 3.3e-172;
  Matches  332;  Conservative   39;  Mismatches   58;  Indels   18;  Gaps   10;

Qy       1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
           |  :|||||  ||||  | |||||||:||||||:|| ||||||  ||||||  |||||||||
Db      27 NQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPDVPAGCRVTFAQVLSRHGARY 86

Qy      59 PTSSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
           || || |||||||| ||:|  || ||||||||||:|||||||||| ::||||||||:|
Db      87 PTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLAD---PAHQASPVINVIIPEGSGY 174
           | || |:| |||||: : ||  |||||:||||:|:  |     || || ::| ||||| |
Db     147 YNALTRHINPFVRATDASRVHESAEKFVEGFQTARQDDHHANPHQPSPRVDVAIPEGSAY 206

Qy     175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
           ||||:| |||||| ||:|||| |||||||| |  |||| |||| |: :|||||| ||||
Db     207 NNTLEHSLCTAFESSTVGDDAVANFTAVFAPAIAQRLEADLPGVQLSTDDVVNLMAMCPF 266

Qy     234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
           :||: | ||  |||||||||| || ||:|| || |||||| |||||| |||| ||||:||
Db     267 ETVSLTDDAHTLSPFCDLFTATEWTQYNYLLSLDKYYGYGGGNPLGPVQGVGWANELMAR 326

Qy     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
           || :|| |||  |:|||::|||||||||||||||||: :||||:|||||||| ||| |||
Db     327 LTRAPVHDHTCVNNTLDASPATFPLNATLYADFSHDSNLVSIFWALGLYNGTAPLSQTSV 386

Qy     351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
           ||: :|||||:|||||||||||||| |       |||||||||||||:|||||  |
Db     387 ESVSQTDGYAAAWTVPFAARAYVEMMQCRA-------EKEPLVRVLVNDRVMPLHGCPTD 439

Qy     410 KLGRCKLDDFVEGLSFARSGGNWAECF 436
           |||||| | || ||||||::|||||:||
Db     440 KLGRCKRDAFVAGLSFAQAGGNWADCF 466


RESULT   6
US-08-744-231-12
; Sequence 12, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-744-231-12


  Query Match             72.7%;  Score 1688;  DB 4;  Length 466;
  Best Local Similarity   74.3%;  Pred. No. 3.3e-172;
  Matches  332;  Conservative   39;  Mismatches   58;  Indels   18;  Gaps   10;

Qy       1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
           |  :|||||  ||||  | |||||||:||||||:|| ||||||  ||||||  |||||||||
Db      27 NQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPDVPAGCRVTFAQVLSRHGARY 86

Qy      59 PTSSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
           || || |||||||| ||:|  || ||||||||||:|||||||||| ::||||||||:|
Db      87 PTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLAD---PAHQASPVINVIIPEGSGY 174
           | || |:| |||||: : ||  |||||:||||:|:  |     || || ::| ||||| |
Db     147 YNALTRHINPFVRATDASRVHESAEKFVEGFQTARQDDHHANPHQPSPRVDVAIPEGSAY 206

Qy     175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
           ||||:| |||||| ||:|||| |||||||| |  |||| |||| |: :|||||| ||||
Db     207 NNTLEHSLCTAFESSTVGDDAVANFTAVFAPAIAQRLEADLPGVQLSTDDVVNLMAMCPF 266

Qy     234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
           :||: | ||  |||||||||| || ||:|| || |||||| |||||| |||| ||||:||
Db     267 ETVSLTDDAHTLSPFCDLFTATEWTQYNYLLSLDKYYGYGGGNPLGPVQGVGWANELMAR 326

Qy     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
           || :|| |||  |:|||::|||||||||||||||||: :||||:|||||||| ||| |||
Db     327 LTRAPVHDHTCVNNTLDASPATFPLNATLYADFSHDSNLVSIFWALGLYNGTAPLSQTSV 386

Qy     351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
           ||: :|||||:|||||||||||||| |       |||||||||||||:|||||  |
Db     387 ESVSQTDGYAAAWTVPFAARAYVEMMQCRA-------EKEPLVRVLVNDRVMPLHGCPTD 439
```

```
Qy     410 KLGRCKLDDFVEGLSFARSGGNWAECF 436
           |||||| | || |||||::||||||:||
Db     440 KLGRCKRDAFVAGLSFAQAGGNWADCF 466


RESULT   7
US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,724
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  1050.0240004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-923-724-8


  Query Match             72.7%;  Score 1688;  DB 1;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 3.3e-172;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy       1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
           |  :|||| |||  | |||||||:||||||:||||||||| |||||| ||||||||||
Db      27 NQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANESAISPDVPAGCRVTFAQVLSRHGARY 86

Qy      59 PTSSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
           || || |||||||| ||:|  || |||||||||||:|||||||||| ::|||||||:|
Db      87 PTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
           |::| |||:||:|:||| ||||| |||||||| || ||     |:|| |:|:| | |
Db     147 YESLTRNIIPFIRSSGSSRVIASGEKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy     175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
           ||||| | || |||| | |  |||||| ||| || |||  | || ||| :|  ||||| |
Db     207 NNTLDPGTCTVFEDSELADTVEANFTATFAPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy     234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
           ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| ||||: ||||||
Db     267 DTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
           |||||| | ||:|||||||||||||:|||||||||| ::|| |||||||||||||||:|
Db     327 LTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy     351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
           |:| :|||:::|||||:| |||||||:|       |:|||||||||||||||| :|
Db     387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPID 439

Qy     410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
           ||||  | || |||||||||:|||| |
Db     440 ALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT   8
US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    APPLICANT:  Houston, Christine S.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,426A
;      FILING DATE:  01-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/923,724
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
```

```
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reed, Grant E.
;      REGISTRATION NUMBER:  P-41,264
;      REFERENCE/DOCKET NUMBER:  1050.008000I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-609-426A-8
```

```
  Query Match             72.7%;  Score 1688;  DB 2;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 3.3e-172;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy       1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
           |  :|||| |||   | ||||||:||||||:||||||||| |||||| ||||||||||
Db      27 NQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANESAISPDVPAGCRVTFAQVLSRHGARY 86

Qy      59 PTSSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
           || || |||||||| ||:|  || ||||||||||:|||||||||| ::||||||||:|
Db      87 PTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
           |::| |||:||:|:||| ||||| |||||||| || ||     |:|| |:|:| | |
Db     147 YESLTRNIIPFIRSSGSSRVIASGEKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy     175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
           ||||| | || |||| | |  |||||| ||| || |||  | || ||| :|  ||||| |
Db     207 NNTLDPGTCTVFEDSELADTVEANFTATFAPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy     234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
           ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| ||||: ||||||
Db     267 DTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
           |||||| | ||:|||||||||||||:|||||||||| ::|| |||||||||||||:|
Db     327 LTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy     351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
           |:| :|||:::::|||||:| |||||||:|       |:||||||||||||||||| :|
Db     387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPID 439

Qy     410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
             ||||  | || |||||||||:|||| |
Db     440 ALGRCTRDSFVRGLSFARSGGDWAECSA 467
```

```
RESULT   9
US-08-374-652C-2
; Sequence 2, Application US/08374652C
; Patent No. 5834286
;  GENERAL INFORMATION:
;    APPLICANT:  NEVALAINEN, HELENA K.M.
;    APPLICANT:  PALOHEIMO, MARJA T.
;    APPLICANT:  FAGERSTROM, RICHARD B.
;    APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;    APPLICANT:  TURUNEN, MARJA K.
;    APPLICANT:  RAMBOSEK, JOHN A.
;    APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;    APPLICANT:  HOUSTON, CHRISTINE S.
;    APPLICANT:  CANTRELL, MICHAEL A.
;    TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;    TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;    TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,652C
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07058
;      FILING DATE:  27-JUL-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/925,401
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REED, GRANT E.
;      REGISTRATION NUMBER:  41,264
;      REFERENCE/DOCKET NUMBER:  1050.071001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-374-652C-2
```

```
  Query Match             72.7%;  Score 1688;  DB 2;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 3.3e-172;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy       1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
           |  :|||| |||   | ||||||:||||||:||||||||| |||||| ||||||||||
Db      27 NQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANESAISPDVPAGCRVTFAQVLSRHGARY 86

Qy      59 PTSSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
           || || |||||||| ||:|  || ||||||||||:|||||||||| ::||||||||:|
Db      87 PTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
           |::| |||:||:|:||| ||||| |||||||| || ||     |:|| |:|:| | |
Db     147 YESLTRNIIPFIRSSGSSRVIASGEKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy     175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
           ||||| | || |||| | |  |||||| ||| || |||  | || ||| :|  ||||| |
Db     207 NNTLDPGTCTVFEDSELADTVEANFTATFAPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy     234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
           ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| ||||: ||||||
Db     267 DTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
           |||||| | ||:|||||||||||||:|||||||||| ::|| |||||||||||||:|
Db     327 LTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy     351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
           |:| :|||:::::|||||:| |||||||:|       |:||||||||||||||||| :|
Db     387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPID 439

Qy     410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
```

```
Db    440 ALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT 10
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,574
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-151-574-32


  Query Match           72.6%;  Score 1684;  DB 1;  Length 467;
  Best Local Similarity  73.9%;  Pred. No. 8.9e-172;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy      1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
          |  |||||| ||||  | |||||||:||||||:|| |||:|| |||||| ||||||||||
Db     27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86

Qy     59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
          || || |||||||| ||:|| || |||||||||||:|||||||||| ::|||||||:|
Db     87 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy    118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
          |::| ||||||:|:||| ||||| :|||||||| || ||      |:|| |:|:| | |
Db    147 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy    175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
          ||||| | || |||| | |  |||||| | | || |||  | || ||| :|  ||||| |
Db    207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy    234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
          ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| ||||: ||||||
Db    267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy    291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
          |||||| | ||:||||||:|||||||:|||||||||| ::|| ||||||||||||||:|
Db    327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy    351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
          |:| :|||:::::|||||:| |||||||:|       |:||||||||||||||||| ||
Db    387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 439

Qy    410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
          ||||  | || ||||||||||:||||||
Db    440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 11
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20


  Query Match           72.6%;  Score 1684;  DB 1;  Length 467;
  Best Local Similarity  73.9%;  Pred. No. 8.9e-172;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy      1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
          |  |||||| ||||  | |||||||:||||||:|| |||:|| |||||| ||||||||||
Db     27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86

Qy     59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
          || || |||||||| ||:|| || |||||||||||:|||||||||| ::|||||||:|
```

```
Db     87 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy    118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
          |::| |||||||:|:||| ||||| :|||||||| || ||     |:|| |:|:| | |
Db    147 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy    175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
          ||||| | || |||| | |  |||||| | | || |||  | || ||| :|  ||||| |
Db    207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy    234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
          ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| ||||: ||||||
Db    267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy    291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
          |||||| | ||:|||||||:|||||||:|||||||||| ::|| |||||||||||||:|
Db    327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy    351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
          |:| :|||::::|||||:| |||||||:|       |:||||||||||||||||| ||
Db    387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 439

Qy    410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
            ||||  | || ||||||||||:|||||
Db    440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 12
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J.J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/693,709
;      FILING DATE:  07-AUG-1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/146,424
;      FILING DATE:  02-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20011.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Signal Sequence
;      LOCATION:  1...23
;      OTHER INFORMATION:
US-08-693-709-2


  Query Match             72.6%;  Score 1684;  DB 1;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 8.9e-172;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy      1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
            |  |||||| |||| | |||||||:||||||:|| |||:|| |||||| ||||||||||
Db     27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86

Qy     59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
          || || |||||||| ||:|| || |||||||||||:|||||||||| ::|||||||:|
Db     87 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy    118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
          |::| ||||||:|:||| ||||| :|||||||| || ||     |:|| |:|:| | |
Db    147 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy    175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
          ||||| | || |||| | |  |||||| | | || |||  | || ||| :|  ||||| |
Db    207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy    234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
          ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| ||||: ||||||
Db    267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy    291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
          |||||| | ||:|||||||:|||||||:|||||||||| ::|| |||||||||||||:|
Db    327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy    351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
          |:| :|||::::|||||:| |||||||:|       |:||||||||||||||||| ||
Db    387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 439

Qy    410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
            ||||  | || ||||||||||:|||||
Db    440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 13
US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

```
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-419-448-32


  Query Match             72.6%;  Score 1684;  DB 2;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 8.9e-172;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy       1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
           |  |||||| ||||  | |||||||:||||||:|| |||:|| |||||| ||||||||||
Db      27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86

Qy      59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
           || || |||||||| ||:|| || ||||||||||:|||||||||| ::|||||||:|
Db      87 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
           |::| ||||||:|:||| ||||| :|||||||| || ||     |:|| |:|:| | |
Db     147 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy     175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
           ||||| | || |||| | |  |||||| | | || |||  | || ||| :|  ||||| |
Db     207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy     234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
           ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| |||| ||||||
Db     267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
           |||||| | ||:|||||:|||||||:|||||||| ::|| |||||||||||||:|
Db     327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy     351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
           |:| :|||:::|||||:| |||||||:|       |:||||||||||||||||| ||
Db     387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 439

Qy     410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
             ||||  | || ||||||||||:||||||
Db     440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  14
US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-825-3


  Query Match             72.6%;  Score 1684;  DB 2;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 8.9e-172;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy       1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
           |  |||||| ||||  | |||||||:||||||:|| |||:|| |||||| ||||||||||
Db      27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86

Qy      59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
           || || |||||||| ||:|| || ||||||||||:|||||||||| ::|||||||:|
Db      87 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
           |::| ||||||:|:||| ||||| :|||||||| || ||     |:|| |:|:| | |
Db     147 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy     175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
           ||||| | || |||| | |  |||||| | | || |||  | || ||| :|  ||||| |
Db     207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy     234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
           ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| |||| ||||||
Db     267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
           |||||| | ||:|||||:|||||||:|||||||| ::|| |||||||||||||:|
Db     327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy     351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
           |:| :|||:::|||||:| |||||||:|       |:||||||||||||||||| ||
Db     387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 439

Qy     410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
             ||||  | || ||||||||||:||||||
Db     440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  15
US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
```

```
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,642
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-163-642-3
```

Query Match 72.6%; Score 1684; DB 4; Length 467;
Best Local Similarity 73.9%; Pred. No. 8.9e-172;
Matches 331; Conservative 40; Mismatches 59; Indels 18; Gaps 10;

```
Qy      1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
          |  |||||| |||| | |||||||:||||||:|| |||:|| |||||| ||||||||||
Db     27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86

Qy     59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
          || || |||||||| ||:|| || |||||||||||:|||||||||| ::||||||||:|
Db     87 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy    118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
          |::| ||||||:|:||| ||||| :|||||||| || ||     |:|| |:|:| | |
Db    147 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy    175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
          ||||| | || |||| | |  |||||| | | || |||  | || ||| :|  ||||| |
Db    207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy    234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
          ||:: ::  |:|||||||| |||  ||||||| ||||:|||||||| ||||: ||||||
Db    267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy    291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
          |||||| | ||:|||||:|||||||:|||||||| ::|| |||||||||||||:|
Db    327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386

Qy    351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
          |:| :|||:::::|||||:| |||||||:|        |:||||||||||||||||| ||
Db    387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 439

Qy    410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
           ||||  | || |||||||||:||||||
Db    440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467
```

Search completed: July 3, 2002, 09:33:13
Job time: 152 sec

OM of: US-09-488-265-28 to: Issued_Patents_AA:* out_format : pfs

Date: Jul 3, 2002 2:38 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09488265/runat_03072002_091241_4286/app_query.fasta_1.4477
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265_@CGN1_1_67 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-488-265-28
Query length: 1404
Database: Issued_Patents_AA:*
Database sequences: 231628
Database length: 24425594
Search time (sec): 54.640000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	!	Documentation
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-1	+	2282.00	4152.17	1.9e-224	441	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-2	+	2270.00	4129.44	3.4e-223	467	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-8	+	1879.00	3412.58	2.9e-183	467	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-8	+	1879.00	3412.58	2.9e-183	467	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2	+	1879.00	3412.58	2.9e-183	467	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-151-574-32	+	1875.00	3405.24	7.4e-183	467	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-146-424-20	+	1875.00	3405.24	7.4e-183	467	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-693-709-2	+	1875.00	3405.24	7.4e-183	467	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-419-448-32	+	1875.00	3405.24	7.4e-183	467	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-3	+	1875.00	3405.24	7.4e-183	467	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-3	+	1875.00	3405.24	7.4e-183	467	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-233-510-32	+	1875.00	3405.24	7.4e-183	467	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-33	+	1867.00	3390.63	4.8e-182	465	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-33	+	1867.00	3390.63	4.8e-182	465	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-3	+	1860.00	3377.74	2.5e-181	467	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-3	+	1860.00	3377.74	2.5e-181	467	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-35	+	1839.00	3339.27	3.5e-179	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-35	+	1839.00	3339.27	3.5e-179	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-29	+	1835.50	3332.94	8.0e-179	463	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-29	+	1835.50	3332.94	8.0e-179	463	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-1	+	1818.00	3301.42	4.7e-177	443	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-1	+	1818.00	3301.42	4.7e-177	443	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-2	+	1813.00	3292.25	1.5e-176	443	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-2	+	1813.00	3292.25	1.5e-176	443	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-12	+	1794.00	3256.77	1.4e-174	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-12	+	1794.00	3256.77	1.4e-174	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-2	+	1761.00	3196.26	3.2e-171	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-2	+	1761.00	3196.26	3.2e-171	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-31	+	1719.00	3119.26	6.3e-167	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-31	+	1719.00	3119.26	6.3e-167	466	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-2	+	1334.00	2413.16	1.3e-127	475	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-2	+	1334.00	2413.16	1.3e-127	475	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-4	+	1313.50	2375.25	1.7e-125	487	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-4	+	1313.50	2375.25	1.7e-125	487	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-30	+	802.50	1439.60	2.4e-73	443	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-24	+	798.50	1432.39	6.1e-73	439	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-09-221-654-2	+	798.50	1432.39	6.1e-73	439	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-989-358A-2	+	798.50	1432.39	6.1e-73	439	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-22	+	795.50	1426.48	1.3e-72	453	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-28	+	781.00	1400.22	3.7e-71	442	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-26	+	778.00	1394.71	7.6e-71	442	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-627-539G-2	+	363.00	633.12	1.9e-28	468	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-627-539G-7	+	358.50	625.49	5.3e-28	446	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-2	+	347.50	604.40	7.3e-27	479	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-2	+	347.50	604.40	7.3e-27	479	!	

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-1

seq_documentation_block:
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

alignment_scores:
Quality: 2282.00 Length: 441
Ratio: 5.234 Gaps: 0
Percent Similarity: 98.866 Percent Identity: 97.732

alignment_block:
US-09-488-265-28 x US-09-121-425-1 ..

Align seg 1/1 to: US-09-121-425-1 from: 1 to: 441

```
 79 AATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGA 128
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGl 17

129 AATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACG 178
    ||||||||||||||||||  ||||||||||||||||||||  ||||
 17 uIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspG 34

179 AATCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTT 228
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 34 luSerAlaIleSerProAspValProAspAspCysArgValThrPheVal 50

229 CAAGTTTTGTCTAGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAA 278
    ||||||||||||||||||||||||||||||||||||||||||  |||||
 51 GlnValLeuSerArgHisGlyAlaArgTyrProThrSerSerLysSerLy 67

279 GGCTTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCA 328
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 67 sAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAlaThrAlaPheL 84

329 AGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 84 ysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

379 GACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGTATTAAGTT 428
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPh 117

429 CTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAG 478
    ||||||||||||||||||||||||||||||||||||||||||||||||||
117 eTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgA 134
```

```
479 CTTCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGT 528
    ||||||||||||||||||||||||||||||||||||||||||||||||||
134 laSerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGly 150

529 TTCCAATCTGCTAAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTC 578
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 PheGlnSerAlaLysLeuAlaAspProGlySerGlnProHisGlnAlaSe 167

579 TCCAGTTATTAACGTGATCATTCCAGAAGGATCCGGTTACAACAACACTT 628
    ||||||||||:::||||||||||||||||||||||||||||||||||||
167 rProValIleAspValIleIleProGluGlySerGlyTyrAsnAsnThrL 184

629 TGGACCACGGTACTTGTACTGCTTTCGAAGACTCTGAATTAGGTGACGAC 678
    ||||||||||||||||||||||||||||||||||||||||||||||||||
184 euAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

679 GTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGAGCTAGATT 728
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLe 217

729 GGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACT 778
    ||||||||||||||||||||||||||||||||||||||||||||||||||
217 uGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrL 234

779 TGATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACT 828
    ||||||||||||||||||||:::||||||||||||||||||||||||||
234 euMetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThr 250

829 GAATTGTCTCCATTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATA 878
    ||||||||||||||||||||||||||||||||||||||||||||  |||||
251 GluLeuSerProPheCysAlaLeuPheThrHisAspGluTrpArgGlnTy 267

879 CGACTACTTGCAAAGCTTGGGTAAGTACTACGGTTACGGTGCTGGTAACC 928
    ||||||||||||||||||||||||||||||||||||||||||||||||||
267 rAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnP 284

929 CATTGGGTCCAGCTCAAGGTGTTGGTTTCGCTAACGAATTGATTGCTAGA 978
    ||||||||||||||||||||||||||||||||||||||||||||||||||
284 roLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

979 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGA 1028
    ||||||:::||||||||||||||||||||||||||||||||||||||||
301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAs 317

1029 CTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCT 1078
     ||||||||||||||||||||||||||||||||||||||||||||||||||
317  pSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheS 334

1079 CTCACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAAC 1128
     ||||||||||:::||||||||||||||||||||||||||||||||||||
334  erHisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsn 350

1129 GGTACCAAGCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGA 1178
     ||||||   ||||||||||||||||||||||||||||||||||||||||
351  GlyThrAlaProLeuSerThrThrSerValGluSerIleGluGluThrAs 367

1179 CGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTG 1228
     ||||||||||||||||||||||||||||||:::||||||||||||||||
367  pGlyTyrSerAlaSerTrpThrValProPheGlyAlaArgAlaTyrValG 384

1229 AAATGATGCAATGTCAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
     ||||||||||||||||||||||||||||||||||||||||||||||||||
384  luMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAGTTGGGTAG 1328
     ||||||||||||||||||||||||||||||||||||||||||||||||||
401  AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyAr 417

1329 ATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTG 1378
     ||||||||||||||||||||||||||||||||||||||||||||||||||
417  gCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyG 434

1379 GTAACTGGGCTGAATGTTTCGCT 1401
```

```
     ||||||||||||||||||||||
434  lyAsnTrpAlaGluCysPheAla 441
```

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-2

seq_documentation_block:
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-2

alignment_scores:
Quality: 2270.00 Length: 487
Ratio: 5.136 Gaps: 2
Percent Similarity: 90.760 Percent Identity: 89.733

alignment_block:
US-09-488-265-28 x US-09-121-425-2 ..

Align seg 1/1 to: US-09-121-425-2 from: 1 to: 467

```
   1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerTh 17

  51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  17 rSerGlyThrAlaLeuGlyProArgGlyAsnSerHisSerCysAspThrV 34

 101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  34 alAspGlyGlyTyrGlnCysPheProGluIleSerHisLeuTrpGlyGln 50

 151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
     ||||||||||||||||||||   ||||||||||||||||||||||||||
  51 TyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAspVa 67

 201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  67 lProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyA 84

 251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
     ||||||||||||||||||   ||||||||||||||||||
  84 laArgTyrProThrSerSerLysSerLysAlaTyrSerAla..... 97

 301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  97 ..... 97

 351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  98 .ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluA 114

 401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 114 snGlnMetValAsnSerGlyIleLysPheTyrArgArgTyrLysAlaLeu 130
```

```
 451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 131 AlaArgLysIleValProPheIleArgAlaSerGlySerAspArgValIl 147

 501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 147 eAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaA 164

 551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAAC..... 591
     ||||||||||||||||||||||||||||||||||||:::
 164 spProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

 591 ..................................................... 591

 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLy 197

 592 .GTGATCATTCCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTA 640
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 197 sValIleIleProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyT 214

 641 CTTGTACTGCTTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAAC 690
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 214 hrCysThrAlaPheGluAspSerGluLeuGlyAspAspValGluAlaAsn 230

 691 TTCACTGCTTTGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTT 740
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 231 PheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAspLe 247

 741 GCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGT 790
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 247 uProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetC 264

 791 GTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
     ||||||||:::||||||||||||||||||||||||||||||||||||||||
 264 ysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

 841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCA 890
     |||||||||||||||||||||||||||||   ||||||||||||||||||
 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGl 297

 891 AAGCTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAG 940
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 297 nSerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProA 314

 941 CTCAAGGTGTTGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCT 990
     ||||||||||||||||||||||||||||||||||||||||||||:::|||
 314 laGlnGlyValGlyPheAlaAsnGluLeuIleAlaArgLeuThrArgSer 330

 991 CCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGC 1040
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 331 ProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnProAl 347

1041 TACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACA 1090
     ||||||||||||||||||||||||||||||||||||||||||||||||:
 347 aThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnS 364

1091 CTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
     ::|||||||||||||||||||||||||||||||||||||||||   |||
 364 erMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGC 1190
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAl 397

1191 TTCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAAT 1240
     ||||||||||||||||||:::|||||||||||||||||||||||||||||
 397 aSerTrpThrValProPheGlyAlaArgAlaTyrValGluMetMetGlnC 414

1241 GTCAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTT 1290
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 414 ysGlnAlaGluLysGluProLeuValArgValLeuValAsnAspArgVal 430
```

```
1291 GTTCCATTGCACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGA 1340
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 431 ValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArgAs 447

1341 CGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTG 1390
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 447 pAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaG 464

1391 AATGTTTCGCT 1401
     ||||||||||
 464 luCysPheAla 467
```

```
seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-8

seq_documentation_block:
; Sequence 8, Application US/07923724
; Patent No. 5780292
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,724
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  1050.0240004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-923-724-8


alignment_scores:
            Quality: 1879.00                Length:    467
```

```
            Ratio:  4.495                Gaps:      0
Percent Similarity:  89.507   Percent Identity: 75.589

alignment_block:
US-09-488-265-28 x US-07-923-724-8   ..

Align seg 1/1  to: US-07-923-724-8  from: 1  to: 467

      1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
        |||||||||   :::||||||||||   :::      |||  |||   ||
      1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

     51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
        |||||||   |||:::           |||:::   :::||||||||||
     17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

    101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
        |||||   ||||||||||||||   |||   ||||||||||||||||
     34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

    151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
        |||:::|||:::|||||||||||||:::|||||||||||||||||||||
     51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

    201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
        ||||      |||||||||||||||:::|||||||||||||||||||||||
     67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

    251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
        ||||||||||||||:::|||   :::|||   ||||||||||||||||||
     84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

    301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
          ||||||:::|||:::|||:::|||   ||||||||||||||||||||
    101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

    351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
        ||||||||||||||:::|||||||||||||||||||||||||||||||:
    117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

    401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
        ::::::::|||||||||||||||||||||||||:::||||||:::::|||
    134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

    451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
        :::|||:::|||:::|||||||||||||:::|||||||||:::||||||||
    151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167

    501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
        |||||||:::|||||||||||||||||||||||||||||||:::||||||   |
    167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

    551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
        |||||   :::||||||   |||:::||||||   |||:::|||:::|||
    184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

    601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
           |||:::|||:::   ||||||||||||||   ||||||||||||::
    201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

    651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
        :|||||||||||||||||:::|||   ||||||||||||||||||||||
    217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

    701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
          |||||||||:::||||||   ||||||||   ||||||   ||||||
    234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

    751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
        ||||||||||||   :::|||:::||||||||||||||||||   |||||
    251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

    801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
        ||||::::::   ::::::      |||:::||||||||||||||||   |
    267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

    851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
        |||||||||||||||||||||||:::|||||||||||||||||||||||
    284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

    901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
        ||||||||||||:::|||||||||||||||||||||||||:::|||||||
    301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

    951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
        ||||:::|||||||||||||||||||||||||||||||||||||||:::|
    317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

   1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
        ||   ||||||:::|||||||||||||||||||||||||||||||||||
    334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

   1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
        ||||||:::|||||||||||||||||||||||||||||   :::||||||
    351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

   1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
        ||||:::|||||||||||||||||||||||||||||||||||||||||||
    367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

   1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
        ||:::|||||:::|||   :::|||||||||:::|||::::::||||||
    384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

   1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
        ||||||||||||:::|||   ||||||||||||||||||||||||||||
    401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

   1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
        |:::||||||||||||||||||||||||||||||||||||||||||||||
    417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

   1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
        ||||||||   :::|||   ||||||||||||   ||||||:::||||||
    434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
        :::|||||||||||||||||||||||||||:::||||||||||||   ||
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

   1401 T 1401
        |
    467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-8

seq_documentation_block:
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    APPLICANT:  Houston, Christine S.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
```

```
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/609,426A
;       FILING DATE:  01-MAR-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/923,724
;       FILING DATE:  31-JUL-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/496,155
;       FILING DATE:  19-MAR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/044,077
;       FILING DATE:  29-APR-1987
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  UK 8610600
;       FILING DATE:  30-APR-1986
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Reed, Grant E.
;       REGISTRATION NUMBER:  P-41,264
;       REFERENCE/DOCKET NUMBER:  1050.008000I
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-609-426A-8


alignment_scores:
            Quality: 1879.00              Length:    467
              Ratio:  4.495                Gaps:      0
 Percent Similarity:  89.507   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-08-609-426A-8   ..

 Align seg 1/1  to: US-08-609-426A-8  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||  |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
         |||||||   |||:::          |||:::   :::||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
         |||||   ||||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||:::||||||||||||:::||||||||||||||||||||||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

     201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||      ||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||

      84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         ||||||:::|||:::|||:::|||   ||||||||||||||||||||
     101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
         ||||||||||||:::|||||||||||||||||||||||||||||||||:
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ::::::::|||||||||||||||||||||||||:::|||||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||:::|||||||||||||:::|||||||||:::|||||||
     151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::|||||||||||||||||||||||||||:::|||||||   |
     167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
         |||||   :::||||||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
           |||:::|||:::   ||||||||||||||   ||||||||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
         :||||||||||||||||:::|||   |||||||||||||||||||||
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
           |||||||||:::||||||   |||||||||   ||||||   ||||||
     234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
         ||||||||||||   :::|||:::||||||||||||||||||   |||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
         ||||::::::   ::::::      |||:::||||||||||||||   |
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
         |||||||||||||||||||||||:::|||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||:::|||||||||||||||||||||||||:::||||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         ||||:::|||||||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
         ||   ||||||:::|||||||||||||||||||||||||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

    1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
         |||||||:::|||||||||||||||||||||||||||||||   :::|||||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
         ||||:::|||||||||||||||||||||||||||||||||||||||||||
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
         ||:::|||||||:::|||   :::|||||||||:::|||:::::::|||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
```

```
   1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
        ||||||||||||:::|||  ||||||||||||||||||||||||||||||
    401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

   1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
        |:::||||||||||||||||||||||||||||||||||||||||||||||
    417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

   1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
        ||||||||   :::|||   ||||||||||||   ||||||:::||||||
    434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
        :::|||||||||||||||||||||||||:::||||||||||||   ||
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

   1401 T 1401
        |
    467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2

seq_documentation_block:
; Sequence 2, Application US/08374652C
; Patent No. 5834286
;  GENERAL INFORMATION:
;    APPLICANT:  NEVALAINEN, HELENA K.M.
;    APPLICANT:  PALOHEIMO, MARJA T.
;    APPLICANT:  FAGERSTROM, RICHARD B.
;    APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;    APPLICANT:  TURUNEN, MARJA K.
;    APPLICANT:  RAMBOSEK, JOHN A.
;    APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;    APPLICANT:  HOUSTON, CHRISTINE S.
;    APPLICANT:  CANTRELL, MICHAEL A.
;    TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;    TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;    TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,652C
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07058
;      FILING DATE:  27-JUL-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/925,401
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REED, GRANT E.
;      REGISTRATION NUMBER:  41,264
;      REFERENCE/DOCKET NUMBER:  1050.071001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-374-652C-2


alignment_scores:
            Quality: 1879.00              Length:    467
              Ratio:  4.495                Gaps:      0
 Percent Similarity:  89.507   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-08-374-652C-2   ..

 Align seg 1/1  to: US-08-374-652C-2  from: 1  to: 467

      1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
        |||||||||   :::||||||||||   :::      |||   |||   ||
      1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

     51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
        |||||||   |||:::            |||:::   :::||||||||||
     17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

    101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
        |||||   ||||||||||||||   |||   ||||||||||||||||
     34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

    151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
        |||:::|||:::||||||||||||:::||||||||||||||||||||||
     51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

    201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
        ||||      ||||||||||||||:::|||||||||||||||||||||||
     67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

    251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
        ||||||||||||||:::|||   :::|||   ||||||||||||||||||
     84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

    301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
           ||||||:::|||:::|||:::|||   ||||||||||||||||||||
    101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

    351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
        ||||||||||||:::|||||||||||||||||||||||||||||||||:
    117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

    401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
        :::::::|||||||||||||||||||||||||:::||||||:::::|||
    134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

    451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
        :::|||:::|||:::|||||||||||||:::|||||||||:::||||||||
    151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167

    501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
        |||||||:::|||||||||||||||||||||||||||:::||||||   |
    167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

    551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
        |||||   :::||||||   |||:::||||||   |||:::|||:::|||
    184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

    601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
           |||:::|||:::   ||||||||||||||   ||||||||||||::
    201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

    651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
        :|||||||||||||||||:::|||   ||||||||||||||||||||||
    217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234
```

```
 701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
     ||||||||||:::||||||  ||||||||  ||||||  ||||||
 234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
     ||||||||||||  :::|||:::||||||||||||||||||  |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
     ||||::::::  ::::::      |||:::||||||||||||||  |
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
     ||||||||||||||||||||||:::||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
     ||||||||||||:::|||||||||||||||||||||||:::||||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
     ||||:::||||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   ||||||:::|||||||||||||||||||||||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
     ||||||:::|||||||||||||||||||||||||||||  :::||||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||:::||||||:::|||   :::||||||||||:::|||:::::||||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
     ||||||||||||:::|||   |||||||||||||||||||||||||||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     |:::||||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||  :::|||  ||||||||||||  |||||||:::||||||
 434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
     :::|||||||||||||||||||||||||:::||||||||||||  ||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

1401 T 1401
     |
 467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-151-574-32

```
seq_documentation_block:
; Sequence 32, Application US/08151574
; Patent No. 5436156
;  GENERAL INFORMATION:
;     APPLICANT:  Robert F.M. Van Gorcom
;     APPLICANT:  Willem Van Hartingsveldt
;     APPLICANT:  Petrus A. Van Paridon
;     APPLICANT:  Annemarie E. Veenstra
;     APPLICANT:  Rudolf G.M. Luttin
;     APPLICANT:  Gerardus Selten
;     TITLE OF INVENTION:  Cloning and Expression of Microbial
;     TITLE OF INVENTION:  Phytase
;     NUMBER OF SEQUENCES:  52
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Morrison & Foerster
;       STREET:  545 Middlefield Road, Suite 200
;       CITY:  Menlo Park
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94025-3471
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;       SOFTWARE:
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/151,574
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/688,578
;       FILING DATE:  24-MAY-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Murashige, Kate H.
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  24615-20026.00
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-327-7250
;  INFORMATION FOR SEQ ID NO:  32:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-151-574-32


alignment_scores:
            Quality: 1875.00                Length:    467
              Ratio:  4.475                   Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-08-151-574-32   ..

 Align seg 1/1  to: US-08-151-574-32  from: 1  to: 467
```

```
   1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
     ||||||||  :::||||||||||  :::      |||  |||  ||
   1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

  51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
     |||||||  |||:::           |||:::  ||||||||||||
  17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

 101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
     |||||  ||||||||||||||  |||  ||||||||||||||||
  34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

 151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
     |||:::|||:::||||||||||||:::||||||:::|||||||||:::||
  51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

 201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
     ||||      ||||||||||||||:::|||||||||||||||||||||
  67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

 251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
     ||||||||||||||:::|||   :::|||   ||||||||||||||||
  84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

 301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
```

```
      ||||||:::|||||||||:::|||   ||||||||||||||||||||
101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
    ||||||||||||:::|||||||||||||||||||||||||||||||||:
117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG. 134

401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
    ::::::::|||||||||||||||||||||||||::||||||::::::|||
134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
    :::|||:::|||||||||||||||||||:::|||||||||:::|||||||
151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
    |||||||:::::|||||||||||||||||||||||||:::||||||   |
167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
    |||||   :::|||||||   |||:::|||||||   |||:::|||:::|||
184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
       |||:::|||:::   ||||||||||||||||   ||||||||||||::
201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
    :|||||||||||||||||:::|||   ||||||||||||||||||||||
217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
       |||:::|||:::||||||   |||||||||   ||||||   ||||||
234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
    ||||||||||||   :::|||:::||||||||||||||||||   |||||
251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
    ||||::::::   ::::::      |||:::|||||||||||||||   |
267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
    ||||||||||||||||||||||:::|||||||||||||||||||||||
284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
    ||||||||||||:::|||||||||||||||||||||||||:::|||||||
301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
    ||||:::|||||||||||||||||||||||||||||||||||||||:::|
317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
     ||||||:::|||||||||||||||||||||||||||||||   :::|||||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||:::||||||:::|||   :::|||||||||:::|||:::::::||||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
     ||||||||||||:::|||   ||||||||||||||||||||||||||||||
```

```
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
         |:::||||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

    1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
         ||||||||   ||||||   ||||||||||||   ||||||:::||||||
     434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

    1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
         :::|||||||||||||||||||||||||:::||||||||||||||||||
     451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

    1401 T 1401
         |
     467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-146-424-20

```
seq_documentation_block:
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20


alignment_scores:
            Quality: 1875.00              Length:    467
              Ratio:  4.475                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-08-146-424-20   ..
```

```
Align seg 1/1  to: US-08-146-424-20  from: 1  to: 467

      1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
        |||||||||   :::|||||||||   :::      |||   |||   ||
      1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

     51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
        |||||||   |||:::           |||:::   ||||||||||||
     17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

    101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
        |||||   ||||||||||||||   |||   ||||||||||||||
     34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

    151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
        |||:::|||:::|||||||||||||:::|||||||::|||||||||:::||
     51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

    201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
        ||||      |||||||||||||||:::|||||||||||||||||||||
     67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

    251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
        ||||||||||||||:::|||   :::|||   ||||||||||||||||||
     84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

    301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
        ||||||:::||||||||||:::|||   ||||||||||||||||||||
    101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

    351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
        ||||||||||||||:::|||||||||||||||||||||||||||||||:
    117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

    401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
        ::::::::|||||||||||||||||||||||:::||||||:::::|||
    134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

    451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
        :::|||:::|||||||||||||||||||:::||||||||||:::||||||||
    151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

    501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
        |||||||::::::|||||||||||||||||||||||||:::||||||   |
    167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

    551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
        |||||   :::|||||||   |||:::|||||||   |||:::|||:::|||
    184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

    601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
           |||:::|||:::   ||||||||||||||||   ||||||||||||::
    201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

    651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
        :|||||||||||||||||:::|||   ||||||||||||||||||||||
    217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

    701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
           |||:::|||:::|||||   |||||||||   ||||||   ||||||
    234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

    751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
        ||||||||||||   :::|||:::|||||||||||||||||||   |||||
    251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

    801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
        ||||::::::   ::::::      |||:::|||||||||||||||   |
    267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

    851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
        ||||||||||||||||||||||::::|||||||||||||||||||||||
    284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

    901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
        ||||||||||||:::|||||||||||||||||||||||||||:::||||||||
    301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

    951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
        ||||:::|||||||||||||||||||||||||||||||||||||||:::|
    317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

   1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
        ||   ||||||:::|||||||||||||||||||:::|||||||||||||
    334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

   1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
        ||||||:::|||||||||||||||||||||||||||||   :::||||||
    351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

   1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
        ||||:::|||||||||||||||||||||||||||||||||||||||||||
    367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

   1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
        ||:::||||||:::|||   :::||||||||||:::|||:::::::||||||
    384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

   1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
        ||||||||||||:::|||   ||||||||||||||||||||||||||||
    401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

   1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
        |:::|||||||||||||||||||||||||||||||||||||||||||||||
    417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

   1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
        ||||||||   ||||||   ||||||||||||   |||||||::||||||
    434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
        :::|||||||||||||||||||||||||||||::||||||||||||||||
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

   1401 T 1401
        |
    467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-693-709-2

seq_documentation_block:
; Sequence 2, Application US/08693709
; Patent No. 5770413
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J.J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  US/08/693,709
;       FILING DATE:  07-AUG-1996
;       CLASSIFICATION:  800
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/146,424
;       FILING DATE:  02-NOV-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Murashige, Kate H
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  24615-20011.10
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-813-5600
;       TELEFAX:  415-494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FRAGMENT TYPE:  internal
;     FEATURE:
;       NAME/KEY:  Signal Sequence
;       LOCATION:  1...23
;       OTHER INFORMATION:
US-08-693-709-2


alignment_scores:
            Quality: 1875.00              Length:    467
              Ratio:  4.475                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-08-693-709-2   ..

 Align seg 1/1  to: US-08-693-709-2  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||  |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
         |||||||   |||:::              |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
         |||||   ||||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||:::||||||||||||:::|||||||:::|||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||      |||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         |||||||:::|||||||||:::|||   ||||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
         ||||||||||||:::|||||||||||||||||||||||||||||||||:
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ::::::::|||||||||||||||||||||||||:::||||||:::::|||

     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::|||||||||:::|||||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::::|||||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
         |||||   :::||||||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
            |||:::|||:::   ||||||||||||||||   ||||||||||||:
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
         :|||||||||||||||||:::|||   |||||||||||||||||||||||
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
            |||:::|||:::||||||   |||||||||   ||||||   ||||||
     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
         ||||||||||||   :::|||:::|||||||||||||||||||   |||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
         ||||::::::   ::::::      |||:::||||||||||||||||   |
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
         ||||||||||||||||||||||:::|||||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||:::|||||||||||||||||||||||||||:::|||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         ||||:::|||||||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
         ||   |||||||:::|||||||||||||||||||:::|||||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

    1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
         ||||||:::|||||||||||||||||||||||||||||||   :::||||||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
         ||||:::|||||||||||||||||||||||||||||||||||||||||||
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
         ||:::|||||:::|||   :::||||||||:::|||:::::|||||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

    1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
         ||||||||||||:::|||   ||||||||||||||||||||||||||||||
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
         |:::|||||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

    1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
         ||||||||   ||||||   ||||||||||||   |||||||:::|||||||
     434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
```

```
     1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
          :::||||||||||||||||||||||||||||||:::||||||||||||||||||
      451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

     1401 T 1401
          |
      467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-419-448-32

```
seq_documentation_block:
; Sequence 32, Application US/08419448
; Patent No. 5863533
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-419-448-32


alignment_scores:
            Quality: 1875.00              Length:    467
              Ratio:  4.475                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-08-419-448-32   ..

 Align seg 1/1  to: US-08-419-448-32  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
         |||||||   |||:::           |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
         |||||   ||||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||:::|||||||||||||:::||||||:::|||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||      ||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         ||||||:::||||||||||:::|||   ||||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
         ||||||||||||:::||||||||||||||||||||||||||||||||||:
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ::::::::|||||||||||||||||||||||||:::||||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::||||||||||:::|||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::::|||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
         |||||   :::||||||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
            |||:::|||:::   ||||||||||||||   ||||||||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
         :||||||||||||||||:::|||   ||||||||||||||||||||||||
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
           |||:::|||:::||||||   |||||||||   ||||||   ||||||
     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
         ||||||||||||   :::|||:::||||||||||||||||||||   |||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
         ||||::::::   ::::::      |||:::||||||||||||||||   |
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
         |||||||||||||||||||||||:::|||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||:::||||||||||||||||||||||||||:::|||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         ||||:::|||||||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334
```

```
1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   |||||||:::|||||||||||||||||||:::||||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
     ||||||:::|||||||||||||||||||||||||||||||   :::|||||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||:::|||||:::|||   :::|||||||||:::|||:::::::||||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
     ||||||||||||:::|||   |||||||||||||||||||||||||||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     |:::||||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||   ||||||   ||||||||||||   ||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
     :::||||||||||||||||||||||||||::||||||||||||||||||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

1401 T 1401
     |
 467 a 467
```

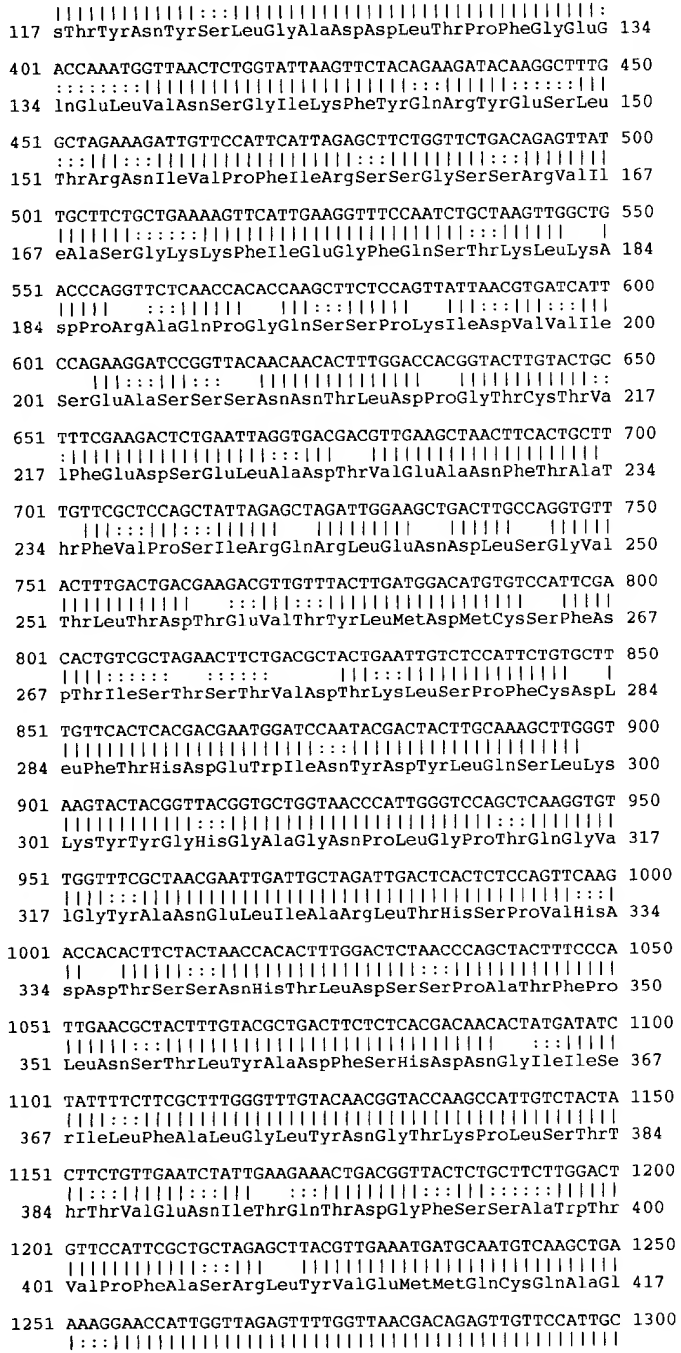
seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-3

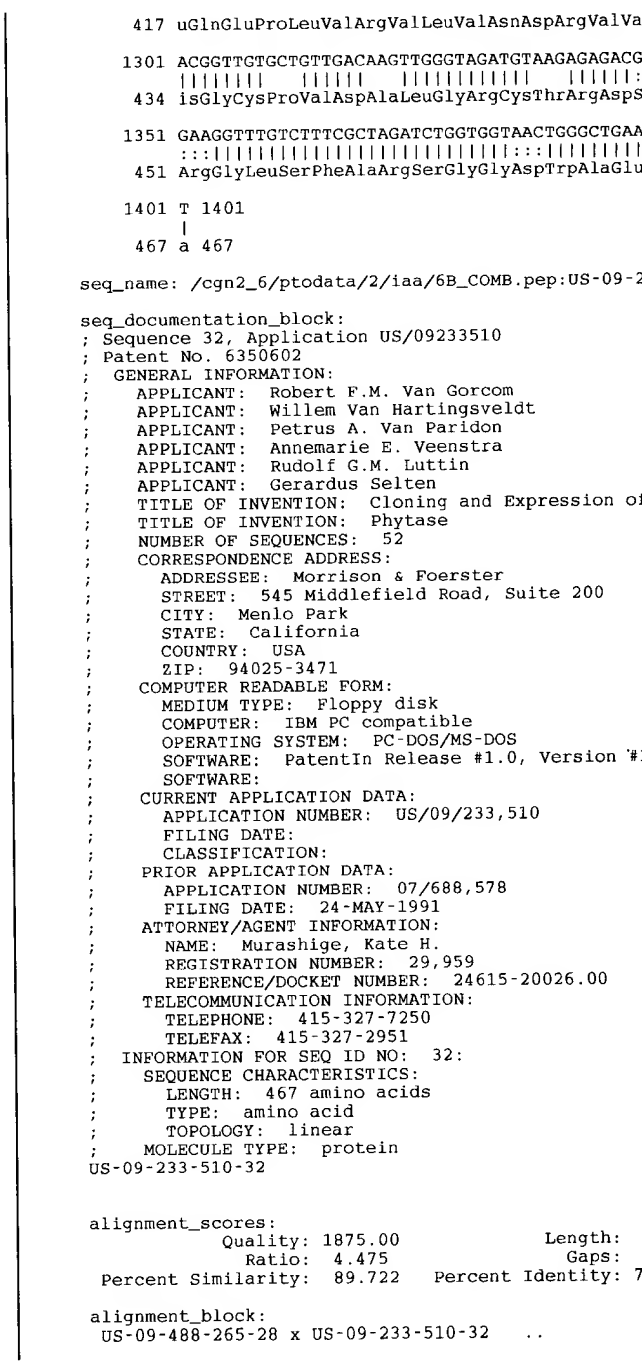
```
seq_documentation_block:
; Sequence 3, Application US/08819825
; Patent No. 5866118
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-825-3


alignment_scores:
           Quality: 1875.00              Length:    467
             Ratio:  4.475                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-08-819-825-3   ..

 Align seq 1/1  to: US-08-819-825-3  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::||||||||||   :::     |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
         |||||||   |||:::            |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
         |||||   ||||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||:::||||||||||||:::||||||:::|||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||      ||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         ||||||:::|||||||||:::|||   ||||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
         ||||||||||||:::|||||||||||||||||||||||||||||||||:
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ::::::::|||||||||||||||||||||||||:::||||||::::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||:::|||||||||:::||||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||::::::|||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
         |||||   :::||||||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
         |||:::|||:::   ||||||||||||||   ||||||||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
         :|||||||||||||||||:::|||   |||||||||||||||||||||
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234
```

```
 701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
     |||:::|||:::||||||   |||||||||   ||||||   ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
     ||||||||||||   :::|||:::|||||||||||||||||||   |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
     ||||::::::   ::::::      |||:::|||||||||||||||   |
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
     ||||||||||||||||||||||:::|||||||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
     ||||||||||||:::|||||||||||||||||||||||||:::||||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
     ||||:::|||||||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
     ||||||:::|||||||||||||||||||||||||||||   :::||||||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||:::|||||||:::|||   :::|||||||||:::|||:::::::|||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
     ||||||||||||:::|||   ||||||||||||||||||||||||||||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     |:::||||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||   ||||||   ||||||||||||   ||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
     :::||||||||||||||||||||||||||:::|||||||||||||||||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

1401 T 1401
     |
 467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-3

```
seq_documentation_block:
; Sequence 3, Application US/09163642
; Patent No. 6221644
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,642
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-163-642-3


alignment_scores:
           Quality: 1875.00              Length:    467
             Ratio:  4.475                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-09-163-642-3   ..

 Align seg 1/1  to: US-09-163-642-3  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
         |||||||   |||:::            |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
         |||||   ||||||||||||||   |||   ||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||:::|||||||||||:::|||||:::|||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||      |||||||||||||||:::|||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
           ||||||:::||||||||||:::|||   ||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
```






```
seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-233-510-32

seq_documentation_block:
; Sequence 32, Application US/09233510
; Patent No. 6350602
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version '#1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/233,510
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-233-510-32


alignment_scores:
            Quality: 1875.00              Length:    467
              Ratio:  4.475                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 75.589

alignment_block:
 US-09-488-265-28 x US-09-233-510-32   ..
```

Align seg 1/1 to: US-09-233-510-32 from: 1 to: 467

```
      1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
        |||||||||   :::|||||||||   :::      |||   |||   ||
      1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

     51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
        |||||||   |||:::            |||:::   ||||||||||||
     17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

    101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
        |||||   ||||||||||||||||   |||   ||||||||||||||
     34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

    151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
        |||:::|||:::|||||||||||||:::||||||:::||||||||:::||
     51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

    201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
        ||||      |||||||||||||||:::|||||||||||||||||||||
     67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

    251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
        ||||||||||||||:::|||   :::|||   ||||||||||||||||||
     84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

    301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
        ||||||:::||||||||||:::|||   ||||||||||||||||||||
    101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

    351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
        |||||||||||||:::|||||||||||||||||||||||||||||||:
    117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

    401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
        ::::::::|||||||||||||||||||||||||:::||||||::::::|||
    134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

    451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
        :::|||:::|||||||||||||||||||:::||||||||||:::||||||||
    151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

    501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
        |||||||:::::|||||||||||||||||||||||||:::||||||   |
    167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

    551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
        |||||   :::||||||   |||:::||||||   |||:::|||:::|||
    184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

    601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
           |||:::|||:::   ||||||||||||||   ||||||||||||::
    201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

    651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
        :|||||||||||||||||:::|||   |||||||||||||||||||||
    217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

    701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
          |||:::|||:::||||||   |||||||||   ||||||   ||||||
    234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

    751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
        ||||||||||||   :::|||:::|||||||||||||||||||   |||||
    251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

    801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
        ||||::::::   ::::::      |||:::|||||||||||||||   |
    267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

    851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
        ||||||||||||||||||||||::|||||||||||||||||||||||||
    284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

    901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
        ||||||||||||:::|||||||||||||||||||||||||:::||||||||
    301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

    951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
        ||||:::|||||||||||||||||||||||||||||||||||||||:::|
    317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

   1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
        ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
    334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

   1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
        ||||||:::|||||||||||||||||||||||||||||||   :::||||||
    351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

   1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
        ||||:::|||||||||||||||||||||||||||||||||||||||||||
    367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

   1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
        ||:::||||||:::|||   :::||||||||||:::|||:::::::||||||
    384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

   1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
        ||||||||||||:::|||   ||||||||||||||||||||||||||||
    401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

   1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
        |:::|||||||||||||||||||||||||||||||||||||||||||||||
    417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

   1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
        ||||||||   ||||||   ||||||||||||   ||||||:::||||||
    434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
        :::|||||||||||||||||||||||||||:::|||||||||||||||||
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

   1401 T 1401
        |
    467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-33

```
seq_documentation_block:
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
```

```
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33


alignment_scores:
            Quality: 1867.00              Length:    467
              Ratio:  4.477                Gaps:      2
 Percent Similarity:  89.293   Percent Identity: 76.017

alignment_block:
 US-09-488-265-28 x US-08-868-435-33   ..

 Align seg 1/1  to: US-08-868-435-33  from: 1  to: 465

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||   :::::::::   |||||||||   |||   |||:::::::::
       1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
             :::::::|||   :::      |||   |||   ||||||||||||
      17 gValSerAlaAlaProSerSerAlaGly...SerLysSerCysAspThrV 33

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
         |||||   ||||||||||||   |||       ||||||||||||||
      33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49

     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
         |||||||||:::|||||||||   ||||||   :::::::|||      ::
      50 TyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLe 66

     201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         :|||   |||||||||:::|||:::||||||||||||||||||||||||
      66 uProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyA 83

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
         ||||||||||||||||||||   ||||||   |||:::   |||:::

      83 laArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         |||||||||   |||||||||   ||||||||||||:::||||||||||||
     100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLy 116

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
         ||||||||||||||||||||||||||||||||||||||||||||||||:
     116 sThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluG 133

     401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ::|||:::|||||||||||||||||||||||:::||||||||||||||||
     133 lnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeu 149

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         ||||||:::::|||||||||||||||||||||||||||||||||||||||
     150 AlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIl 166

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::|||||||||||||||||||||||:::||||||||||||||
     166 eAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaA 183

     551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
         |||||||||:::      ::::::|||:::|||:::|||:::|||||||||
     183 spProGlyAla...ThrAsnArgAlaAlaProAlaIleSerValIleIle 198

     601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
         ||||||::::::   :::|||||||||||||||||||:::||||||
     199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLy 215

     651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
          ||||||   |||:::|||||||||:::|||   |||||||||||||||
     215 sPheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaL 232

     701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
         ||||||||||||   ||||||||||||   |||      ||||||||||||
     232 euPheAlaProAspIleArgAlaArgAlaGluLysHisLeuProGlyVal 248

     751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
         ||||||||||||||||||||||||   ||||||||||||||||   |||||
     249 ThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAs 265

     801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
         ||||||||||||||||||||||||:::::::||||||||||||||||   |
     265 pThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnL 282

     851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
         ||||||||||||:::|||||||   :::|||:::||||||||||||||||||
     282 euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||||||||||||||||||||||||||||||||||||||||::
     299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl 315

     951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         :|||||:::|||||||||||||||||||||||||:::|||||||||||||
     315 eGlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnA 332

    1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
         ||||||||||||||||   ||||||   ||||||||||||||||||||||
     332 spHisThrSerThrAsnSerThrLeuValSerAsnProAlaThrPhePro 348

    1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
         ||||||||||||:::|||:::||||||||||||||||||:::|||:::||
     349 LeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSe 365

    1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
         ||||||||||||||||||||||||||||||||:::|||||||||   |
     365 rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382

    1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
         ||||||||||||||   :::|||   ||||||||||||||||||||:::
     382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
```

```
    1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
         |||||||||:::|||||||||||||   |||  ,||||||||:::::||
     399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGl 415

    1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
         ||||||||||||||||||:::|||:::||||||||||||||||||||||
     415 uLysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuH 432

    1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
         ||||||||   ||||||||||||||||||||||   :::|||||||||
     432 isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448

    1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
         :::||||||||||:::|||||||||||||||||||||:::|||||||||::
     449 LysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSe 465

    1401 T 1401
         :
     465 r 465

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-33

seq_documentation_block:
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33


alignment_scores:
            Quality: 1867.00            Length:    467
              Ratio:  4.477              Gaps:      2
 Percent Similarity:  89.293   Percent Identity: 76.017

alignment_block:
 US-09-488-265-28 x US-08-744-231-33   ..

 Align seg 1/1  to: US-08-744-231-33  from: 1  to: 465

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||   :::::::::   |||||||||   |||   |||::::::::::
       1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
             ::::::|||   :::      |||   |||   ||||||||||||
      17 gValSerAlaAlaProSerSerAlaGly...SerLysSerCysAspThrV 33

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
         |||||   ||||||||||||   |||      ||||||||||||||||
      33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49

     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
         ||||||||||:::|||||||||   ||||||   :::::::|||      ::
      50 TyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLe 66

     201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         :|||   |||||||||:::||:::||||||||||||||||||||||||||
      66 uProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyA 83

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
         ||||||||||||||||||   ||||||   |||:::   |||:::
      83 laArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         |||||||||   |||||||||   ||||||||||||:::||||||||||
     100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLy 116

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
         ||||||||||||||||||||||||||||||||||||||||||||||||:
     116 sThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluG 133

     401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ::|||:::||||||||||||||||||||||:::||||||||||||||||
     133 lnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeu 149

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         ||||||::::::|||||||||||||||||||||||||||||||||||||
     150 AlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIl 166

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::|||||||||||||||||||||||:::||||||||||||||
     166 eAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaA 183

     551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
         |||||||||:::      ::::::|||:::|||:::|||:::|||||||||
```

```
 183 spProGlyAla...ThrAsnArgAlaAlaProAlaIleSerValIleIle 198

 601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
     ||||||::::::   :::||||||||||||||||||||||:::||||||
 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLy 215

 651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
      ||||||   |||:::|||||||||:::|||   ||||||||||||||||
 215 sPheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaL 232

 701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
     ||||||||||   ||||||||||||   |||      ||||||||||||
 232 euPheAlaProAspIleArgAlaArgAlaGluLysHisLeuProGlyVal 248

 751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
     ||||||||||||||||||||||||   ||||||||||||||   |||||
 249 ThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAs 265

 801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
     ||||||||||||||||||||||||||::::::|||||||||||||||   |
 265 pThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnL 282

 851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
     ||||||||||:::||||||   :::|||:::|||||||||||||||||||
 282 euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
     ||||||||||||||||||||||||||||||||||||||||||||||||::
 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl 315

 951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
     :|||||||:::|||||||||||||||||||||||||:::||||||||||||
 315 eGlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnA 332

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||||||||||||||||   ||||||   ||||||||||||||||||||||
 332 spHisThrSerThrAsnSerThrLeuValSerAsnProAlaThrPhePro 348

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
     ||||||||||||:::|||:::|||||||||||||||||||:::|||:::||
 349 LeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSe 365

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
     ||||||||||||||||||||||||||||||||||:::|||||||||   |
 365 rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||||||||||||||   :::|||   ||||||||||||||||||||:::
 382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
     |||||||||:::||||||||||||   |||   |||||||||:::::||
 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGl 415

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     ||||||||||||||||||:::|||:::||||||||||||||||||||||
 415 uLysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuH 432

1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||   ||||||||||||||||||||||   :::|||||||||
 432 isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
     :::||||||||||:::|||||||||||||||||||||||:::|||||||::
 449 LysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSe 465

1401 T 1401
     :
 465 r 465

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-3

seq_documentation_block:
```

```
; Sequence 3, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
;  APPLICANT: KONDO, Hidemasa
;  APPLICANT: ANAZAWA, Hideharu
;  APPLICANT: KANEKO, Syunichi
;  APPLICANT: NAGASHIMA, Tadashi
;  APPLICANT: TANGE, Tatsuya
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 81356/124
;  CURRENT APPLICATION NUMBER: US/09/155,855
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
;  EARLIER FILING DATE: 1997-04-04
;  EARLIER APPLICATION NUMBER: JP 084314
;  EARLIER FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-155-855-3


alignment_scores:
           Quality: 1860.00              Length:    467
             Ratio:  4.418                Gaps:      0
 Percent Similarity:  90.150   Percent Identity: 74.090

alignment_block:
 US-09-488-265-28 x US-09-155-855-3   ..

 Align seg 1/1  to: US-09-155-855-3  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
         |||||||   |||:::            |||:::   :::||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
         |||||   ||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||:::|||||||||||:::::|||||||||||||||||||||
      51 TyrAlaProPhePheSerLeuAlaAsnLysSerAlaIleSerProAspVa 67

     201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||      |||:::|||||||||:::|||||||||||||||||||||
      67 lProAlaGlyCysHisValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         |||||||:::|||||||||:::|||:::|||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
         ||||||||||||:::|||||||||||||||||||||||||||||||||:
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         :::::::|||||||||||||:::|||||||||:::|||||::::::|||
     134 lnGluLeuValAsnSerGlyValLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::|||||||||:::|||||||
```

```
 151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

 501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
     |||||||:::::|||||||||||||||||||||||||||:::||||||   |
 167 eAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

 551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
     |||||   :::||||||   |||:::||||||   |||:::|||:::|||
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
       |||:::|||       ||||||||||||||   ||||||||||||::
 201 SerGluAlaSerThrSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
     :|||||||||||||||||:::||||||:::|||||||||||||||||||
 217 lPheGluAspSerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaT 234

 701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
       |||:::|||:::||||||   |||||||||   ||||||   ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
     :::|||||||||   :::|||:::|||||||||||||||||||   |||||
 251 SerLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
     ||||::::::   ::::::      |||:::|||||||||||||||   |
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
     ||||||||||||:::|||||||||:::|||||||||||||||||||||:::
 284 euPheThrHisGluGluTrpIleAsnTyrAspTyrLeuGlnSerLeuAsn 300

 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
     ||||||||||||:::|||||||||||||||||||||||||||:::|||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
     ||||:::|||||||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   ||||||:::|||||||||||||||||||||||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
     ||||||:::|||||||||||||||||||||||||||||||   :::|||||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||:::|
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerSerT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||:::::|||:::|||   :::|||||||||:::|||:::::|||||||
 384 hrThrAlaGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
     ||||||||||||:::|||   |||||||||||||||||||||||:::||
 401 ValProPheAlaSerArgMetTyrValGluMetMetGlnCysGlnSerGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     |:::|||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||   ||||||   ||||||||||||   |||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1400
     :::|||||||||||||||||||||||||||||:::|||:::||||||||||
 451 LysGlyLeuSerPheAlaArgSerGlyGlyAspTrpGlyGluCysPheAl 467
```

```
1401 T 1401
     |
 467 a 467
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 3, 2002, 09:33:13 ; Search time 39.56 Seconds
(without alignments)
288.341 Million cell updates/sec

Title: US-09-488-265-29
Perfect score: 2462
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWAECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2282	92.7	441	4	US-09-121-425-1	Sequence 1, Appli
2	2270	92.2	467	4	US-09-121-425-2	Sequence 2, Appli
3	1879	76.3	467	1	US-07-923-724-8	Sequence 8, Appli
4	1879	76.3	467	2	US-08-609-426A-8	Sequence 8, Appli
5	1879	76.3	467	2	US-08-374-652C-2	Sequence 2, Appli
6	1875	76.2	467	1	US-08-151-574-32	Sequence 32, Appl
7	1875	76.2	467	1	US-08-146-424-20	Sequence 20, Appl
8	1875	76.2	467	1	US-08-693-709-2	Sequence 2, Appli
9	1875	76.2	467	2	US-08-419-448-32	Sequence 32, Appl
10	1875	76.2	467	2	US-08-819-825-3	Sequence 3, Appli
11	1875	76.2	467	4	US-09-163-642-3	Sequence 3, Appli
12	1875	76.2	467	4	US-09-233-510-32	Sequence 32, Appl
13	1867	75.8	465	4	US-08-868-435-33	Sequence 33, Appl
14	1867	75.8	465	4	US-08-744-231-33	Sequence 33, Appl
15	1860	75.5	467	4	US-09-155-855-3	Sequence 3, Appli
16	1860	75.5	467	4	US-09-543-744-3	Sequence 3, Appli
17	1839	74.7	466	4	US-08-868-435-35	Sequence 35, Appl
18	1839	74.7	466	4	US-08-744-231-35	Sequence 35, Appl
19	1835.5	74.6	463	4	US-08-868-435-29	Sequence 29, Appl
20	1835.5	74.6	463	4	US-08-744-231-29	Sequence 29, Appl
21	1818	73.8	443	4	US-09-155-855-1	Sequence 1, Appli
22	1818	73.8	443	4	US-09-543-744-1	Sequence 1, Appli
23	1813	73.6	443	4	US-09-155-855-2	Sequence 2, Appli
24	1813	73.6	443	4	US-09-543-744-2	Sequence 2, Appli
25	1794	72.9	466	4	US-08-868-435-12	Sequence 12, Appl
26	1794	72.9	466	4	US-08-744-231-12	Sequence 12, Appl
27	1761	71.5	466	4	US-08-868-435-2	Sequence 2, Appli
28	1761	71.5	466	4	US-08-744-231-2	Sequence 2, Appli
29	1719	69.8	466	4	US-08-868-435-31	Sequence 31, Appl
30	1719	69.8	466	4	US-08-744-231-31	Sequence 31, Appl
31	1334	54.2	475	2	US-08-819-825-2	Sequence 2, Appli
32	1334	54.2	475	4	US-09-163-642-2	Sequence 2, Appli
33	1313.5	53.4	487	4	US-08-868-435-4	Sequence 4, Appli
34	1313.5	53.4	487	4	US-08-744-231-4	Sequence 4, Appli
35	802.5	32.6	443	3	US-08-993-359-30	Sequence 30, Appl
36	798.5	32.4	439	3	US-08-993-359-24	Sequence 24, Appl
37	798.5	32.4	439	3	US-09-221-654-2	Sequence 2, Appli
38	798.5	32.4	439	3	US-08-989-358A-2	Sequence 2, Appli
39	795.5	32.3	453	3	US-08-993-359-22	Sequence 22, Appl
40	781	31.7	442	3	US-08-993-359-28	Sequence 28, Appl
41	778	31.6	442	3	US-08-993-359-26	Sequence 26, Appl
42	363	14.7	468	1	US-07-627-539G-2	Sequence 2, Appli
43	358.5	14.6	446	1	US-07-627-539G-7	Sequence 7, Appli
44	347.5	14.1	479	1	US-07-923-724-2	Sequence 2, Appli
45	347.5	14.1	479	2	US-08-609-426A-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT   1
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

  Query Match             92.7%;  Score 2282;  DB 4;  Length 441;
  Best Local Similarity   97.7%;  Pred. No. 1.2e-230;
  Matches  431;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      27 NSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARY 86
           ||||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||||
Db       1 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 60

Qy      87 PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 146
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 PTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

Qy     147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGY 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db     121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy     207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

Qy     267 DTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 326
           :||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     241 ETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300

Qy     327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 386
           || ||||||||||||||||||||||||||||||:|||||||||||||| |||||||
```

```
Db    301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy    387 ESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 446
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy    447 DDFVEGLSFARSGGNWAECFA 467
          |||||||||||||||||||||
Db    421 DDFVEGLSFARSGGNWAECFA 441


RESULT   2
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2


  Query Match             92.2%;  Score 2270;  DB 4;  Length 467;
  Best Local Similarity   89.7%;  Pred. No. 2.4e-229;
  Matches  437;  Conservative    3;  Mismatches    7;  Indels   40;  Gaps    2;

Qy      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||
Db      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy     61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
          |||||||||||||||||||||||||||||| ||||||                   |||
Db     61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSA--------------------TYN 100

Qy    121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160

Qy    181 KLADPGSQPHQASPVIN-------------------VIIPEGSGYNNTLDHGTCTAFED 220
          |||||||||||||||:                   ||||||||||||||||||||||
Db    161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy    221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSP 280
          |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db    221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

Qy    281 FCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
          |||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||||
Db    281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy    341 TLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWT 400
          |||||||||||||||||||:|||||||||||| ||||||||||||||||||||||||||||
Db    341 TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

Qy    401 VPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460

Qy    461 NWAECFA 467
          |||||||
Db    461 NWAECFA 467


RESULT   3
US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,724
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  1050.0240004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-923-724-8


  Query Match             76.3%;  Score 1879;  DB 1;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 2.4e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
          |||  ||| :  | | ||| |:    |  :|||| ||||| | ||||| |:|:||||:|
Db      1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy     61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
          ||||||||  ||||| ||||||||||||| |  | ||||||  ||:| | | ||||||||||
Db     61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
```

```
Qy    121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db    121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy    181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db    181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy    241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db    241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy    301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db    301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy    361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db    361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy    421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
Db    421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467
```

```
RESULT   4
US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;     APPLICANT:  Nevalainen, Helena K.M.
;     APPLICANT:  Paloheimo, Marja T.
;     APPLICANT:  Miettinen-Oinonen, Arja S.K.
;     APPLICANT:  Torkkeli, Tuula K.
;     APPLICANT:  Cantrell, Michael
;     APPLICANT:  Piddington, Christopher S.
;     APPLICANT:  Rambosek, John A.
;     APPLICANT:  Turunen, Marja K.
;     APPLICANT:  Fagerstr m, Richard B.
;     APPLICANT:  Houston, Christine S.
;     TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;     TITLE OF INVENTION:  in Trichoderma
;     NUMBER OF SEQUENCES:  69
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;       STREET:  1100 New York Avenue, Suite 600
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/609,426A
;       FILING DATE:  01-MAR-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/923,724
;       FILING DATE:  31-JUL-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/496,155
;       FILING DATE:  19-MAR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/044,077
;       FILING DATE:  29-APR-1987
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  UK 8610600
;       FILING DATE:  30-APR-1986
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Reed, Grant E.
;       REGISTRATION NUMBER:  P-41,264
;       REFERENCE/DOCKET NUMBER:  1050.008000I
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-609-426A-8


  Query Match           76.3%;  Score 1879;  DB 2;  Length 467;
  Best Local Similarity  75.6%;  Pred. No. 2.4e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db      1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy     61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db     61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy    121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db    121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy    181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db    181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy    241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db    241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy    301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db    301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy    361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db    361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy    421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
Db    421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467
```

```
RESULT   5
US-08-374-652C-2
; Sequence 2, Application US/08374652C
; Patent No. 5834286
;  GENERAL INFORMATION:
;     APPLICANT:  NEVALAINEN, HELENA K.M.
;     APPLICANT:  PALOHEIMO, MARJA T.
;     APPLICANT:  FAGERSTROM, RICHARD B.
;     APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;     APPLICANT:  TURUNEN, MARJA K.
;     APPLICANT:  RAMBOSEK, JOHN A.
;     APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;     APPLICANT:  HOUSTON, CHRISTINE S.
;     APPLICANT:  CANTRELL, MICHAEL A.
;     TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;     TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;     TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;     NUMBER OF SEQUENCES:  94
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;       STREET:  1100 NEW YORK AVENUE, SUITE 600
;       CITY:  WASHINGTON
```

```
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,652C
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07058
;      FILING DATE:  27-JUL-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/925,401
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REED, GRANT E.
;      REGISTRATION NUMBER:  41,264
;      REFERENCE/DOCKET NUMBER:  1050.071001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-374-652C-2


  Query Match             76.3%;  Score 1879;  DB 2;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 2.4e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
           |||  ||| :  | | ||| |:    |  :|||| |||| | |||| |:|:||||:|
Db       1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           ||||||||  ||||| ||||||||||||  |  | |||||| ||:| | | ||||||||||
Db      61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||| ::|||||||:||::| | |:||||:||| ||||| |||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
           || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| |||:||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
           ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| ||||:||||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
           ||| :||| |||||||||||||||:||:| :|||:|::|||||:| ||||||||||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
           |||||||||||||| :| |||| || || ||||||||:|||| |
Db     421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467
```

```
RESULT   6
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,574
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-151-574-32


  Query Match             76.2%;  Score 1875;  DB 1;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 6.3e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| |||| | |||| |:|:||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:||  ||||| |||||||||||  |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||| ::|||||||:||::| | |||||:||| ||||| :|||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
           || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| | |:||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
           ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
```

```
Qy    301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
          ||||:|||||||| ||||:||||||||||||| | ||:||||||:|||||||:|||||||
Db    301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy    361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
          ||| :||| |||||||||||||||:||:| :|||:|::||||||:| ||||||||||:||
Db    361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy    421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
          |||||||||||||| || |||| || || ||||||||:||||||
Db    421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT   7
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20


  Query Match             76.2%;  Score 1875;  DB 1;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 6.3e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
            |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|:|||||:|
Db      1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy     61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
          | |||:||  ||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db     61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy    121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
          |:|||||||||| ::|||||||:||::| | ||||||:||| ||||| :|||||||
Db    121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy    181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
          || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| | |:||
Db    181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy    241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
          ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db    241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy    301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
          ||||:|||||||| ||||:||||||||||||| | ||:||||||:|||||||:|||||||
Db    301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy    361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
          ||| :||| |||||||||||||||:||:| :|||:|::||||||:| ||||||||||:||
Db    361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy    421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
          |||||||||||||| || |||| || || ||||||||:||||||
Db    421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT   8
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J.J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/693,709
;      FILING DATE:  07-AUG-1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/146,424
;      FILING DATE:  02-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20011.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
```

```
;    FEATURE:
;      NAME/KEY:  Signal Sequence
;      LOCATION:  1...23
;      OTHER INFORMATION:
US-08-693-709-2


  Query Match             76.2%;  Score 1875;  DB 1;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 6.3e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|:||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:||  ||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||| ::|||||||:||::| | ||||||:||| ||||| :|||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
           || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| | |:||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
           ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| ||||:||||||||||||| | ||:|||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
           ||| :||| |||||||||||||||:||:| :|||:|::|||||:| ||||||||||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
           |||||||||||||| || |||| || || ||||||||:||||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT   9
US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-419-448-32


  Query Match             76.2%;  Score 1875;  DB 2;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 6.3e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|:||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:||  ||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||| ::|||||||:||::| | ||||||:||| ||||| :|||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
           || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| | |:||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
           ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| ||||:||||||||||||| | ||:|||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
           ||| :||| |||||||||||||||:||:| :|||:|::|||||:| ||||||||||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
           |||||||||||||| || |||| || || ||||||||:||||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  10
US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/819,825
;       FILING DATE:  18-MAR-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lambiris, Elias J.
;       REGISTRATION NUMBER:  33,728
;       REFERENCE/DOCKET NUMBER:  4758.200-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212 867 0123
;       TELEFAX:  212 867 0298
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-819-825-3


  Query Match             76.2%;  Score 1875;  DB 2;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 6.3e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  11
US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,642
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-163-642-3


  Query Match             76.2%;  Score 1875;  DB 4;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 6.3e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  12
US-09-233-510-32
```

```
; Sequence 32, Application US/09233510
; Patent No. 6350602
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/233,510
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-233-510-32


  Query Match             76.2%;  Score 1875;  DB 4;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 6.3e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|:||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:||  ||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||| ::|||||||:||::| | |||||:||| ||||| :||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
           || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| | |:||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
           ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           |||:||||||| |||:|||||||||||| | ||:|||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
           ||| :||| |||||||||||||:||:| :|||:|::|||||:| ||||||||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
           |||||||||||||| || |||| || || |||||||||:||||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  13
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
```

```
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33


  Query Match             75.8%;  Score 1867;  DB 4;  Length 465;
  Best Local Similarity   76.0%;  Pred. No. 4.3e-187;
  Matches  355;  Conservative   36;  Mismatches   74;  Indels    2;  Gaps    2;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
           |     ||| | |       |    | | |||||| |||| |  ||||| |||:||| ||
Db       1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
             ::|  :| |||:| |||||||||||||||| || |  |: ||| ||| ||||:|||||||
Db      60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           ||||||||||||| |:||||||||:|||||| :|||||||||||||| |||||||| |
Db     120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
           ||||||:  ::|:| |:|||||   :|||||| || || |:|||:| |||||||| ||
Db     180 KLADPGA-TNRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
           || |  |||||||||||| ||||| |||||||||::||||| ||||:|| :|:||||||
Db     239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db     299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
           |||:|:|||||||||||:||| ||||| :| ||||||| ||| |||| | |||::||||
Db     359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
           ||| |:|||||||||| |||||||| :|||:|||:||||||| |||:
Db     419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT  14
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33


  Query Match             75.8%;  Score 1867;  DB 4;  Length 465;
  Best Local Similarity   76.0%;  Pred. No. 4.3e-187;
  Matches  355;  Conservative   36;  Mismatches   74;  Indels    2;  Gaps    2;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
           |     ||| | |       |    | | |||||| |||| |  ||||| |||:||| ||
Db       1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
             ::|  :| |||:| |||||||||||||||| || |  |: ||| ||| ||||:|||||||
Db      60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           ||||||||||||| |:||||||||:|||||| :|||||||||||||| |||||||| |
Db     120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
           ||||||:  ::|:| |:|||||   :|||||| || || |:|||:| |||||||| ||
Db     180 KLADPGA-TNRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
           || |  |||||||||||| ||||| |||||||||::||||| ||||:|| :|:||||||
Db     239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db     299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
           |||:|:|||||||||||:||| ||||| :| ||||||| ||| |||| | |||::||||
Db     359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
           ||| |:|||||||||| |||||||| :|||:|||:||||||| |||:
Db     419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
```

```
Db    419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 15
US-09-155-855-3
; Sequence 3, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
;  APPLICANT: KONDO, Hidemasa
;  APPLICANT: ANAZAWA, Hideharu
;  APPLICANT: KANEKO, Syunichi
;  APPLICANT: NAGASHIMA, Tadashi
;  APPLICANT: TANGE, Tatsuya
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 81356/124
;  CURRENT APPLICATION NUMBER: US/09/155,855
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
;  EARLIER FILING DATE: 1997-04-04
;  EARLIER APPLICATION NUMBER: JP 084314
;  EARLIER FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-155-855-3


  Query Match             75.5%;  Score 1860;  DB 4;  Length 467;
  Best Local Similarity   74.1%;  Pred. No. 2.4e-186;
  Matches  346;  Conservative   48;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:|:||||::
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANK 60

Qy      61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           ||||||||  | ||| ||||||||||||| |  | ||||| ||:||| |:|||||||||
Db      61 SAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFEGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||| ::|||:|||:||::| | ||||||:||| |||||  ||||||||
Db     121 YSLGADDLTPFGEQELVNSGVKFYQRYESLTRNIVPFIRSSGSSRVIASGNKFIEGFQST 180

Qy     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
           || || :|| |:|| |:|:| | |  ||||| |||| |||||| ||:|||||| | |:||
Db     181 KLKDPRAQPGQSSPKIDVVISEASTSNNTLDPGTCTVFEDSELADDIEANFTATFVPSIR 240

Qy     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
            ||| || ||:||| :| |||||| |||:: ::  |:||||| ||||:||| |||||||
Db     241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHEEWINYDYLQSLN 300

Qy     301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||:|||||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
           ||| :||| |||||||||||||:|: |:| :|||:|::|||||||:| |||||||||:|:||
Db     361 HDNGIISILFALGLYNGTKPLSSTTAENITQTDGFSSAWTVPFASRMYVEMMQCQSEQEP 420

Qy     421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
           |||||||||||||||| || |||| || ||:||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVKGLSFARSGGDWGECFA 467


Search completed: July  3, 2002, 09:33:14
Job time: 153 sec
```

OM of: US-09-488-265-30 to: Issued_Patents_AA:* out_format : pfs

Date: Jul 3, 2002 2:39 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09488265/runat_03072002_091241_4286/app_query.fasta_1.4477
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265_@CGN1_1_67 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-488-265-30
Query length: 1404
Database: Issued_Patents_AA:*
Database sequences: 231628
Database length: 24425594
Search time (sec): 54.640000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	!	Documentation
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-1	+	2182.00	3827.52	2.4e-206	441	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-2	+	2170.00	3805.58	3.7e-205	467	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-33	+	1888.00	3307.19	2.2e-177	465	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-33	+	1888.00	3307.19	2.2e-177	465	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-8	+	1852.00	3243.51	7.6e-174	467	!	S
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-8	+	1852.00	3243.51	7.6e-174	467	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2	+	1852.00	3243.51	7.6e-174	467	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-151-574-32	+	1848.00	3236.44	1.9e-173	467	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-146-424-20	+	1848.00	3236.44	1.9e-173	467	!	
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-693-709-2	+	1848.00	3236.44	1.9e-173	467	!	S
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-419-448-32	+	1848.00	3236.44	1.9e-173	467	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-3	+	1848.00	3236.44	1.9e-173	467	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-3	+	1848.00	3236.44	1.9e-173	467	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-233-510-32	+	1848.00	3236.44	1.9e-173	467	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-3	+	1841.00	3224.06	9.1e-173	467	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-3	+	1841.00	3224.06	9.1e-173	467	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-35	+	1822.00	3190.51	6.8e-171	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-35	+	1822.00	3190.51	6.8e-171	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-12	+	1819.00	3185.20	1.3e-170	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-12	+	1819.00	3185.20	1.3e-170	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-29	+	1804.50	3159.66	3.6e-169	463	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-29	+	1804.50	3159.66	3.6e-169	463	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-1	+	1799.00	3150.49	1.2e-168	443	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-1	+	1799.00	3150.49	1.2e-168	443	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-2	+	1794.00	3141.66	3.8e-168	443	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-543-744-2	+	1794.00	3141.66	3.8e-168	443	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-2	+	1752.00	3066.78	5.3e-164	466	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-2	+	1752.00	3066.78	5.3e-164	466	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-31	+	1710.00	2992.54	7.2e-160	466	!	
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-31	+	1710.00	2992.54	7.2e-160	466	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-2	+	1381.00	2410.78	1.8e-127	475	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-2	+	1381.00	2410.78	1.8e-127	475	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-4	+	1334.50	2328.28	6.9e-123	487	!	S
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-4	+	1334.50	2328.28	6.9e-123	487	!	S
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-30	+	845.50	1465.15	9.0e-75	443	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-22	+	833.50	1443.66	1.4e-73	453	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-24	+	830.50	1438.75	2.7e-73	439	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-09-221-654-2	+	830.50	1438.75	2.7e-73	439	!	S
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-989-358A-2	+	830.50	1438.75	2.7e-73	439	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-28	+	825.00	1428.95	9.4e-73	442	!	
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-993-359-26	+	814.00	1409.50	1.1e-71	442		
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-627-539G-2	+	359.00	604.56	7.4e-27	468		
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-627-539G-7	+	354.50	597.21	2.0e-26	446		
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-2	+	354.50	596.31	2.1e-26	479	!	
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-2	+	354.50	596.31	2.1e-26	479		

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-1

seq_documentation_block:
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

alignment_scores:
Quality: 2182.00 Length: 441
Ratio: 5.098 Gaps: 0
Percent Similarity: 97.052 Percent Identity: 92.971

alignment_block:
US-09-488-265-30 x US-09-121-425-1 ..

Align seg 1/1 to: US-09-121-425-1 from: 1 to: 441

```
     79 AACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGA 128
        ||||||||||||||||||||||||||||||||||||||||||||||||||
      1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGl 17

    129 AATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACG 178
        |||||||||||||||||||    ||||||||:::|||||||||    ||||
     17 uIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspG 34

    179 AATCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTT 228
        ||||||||||||||||||||||||||      ||||||||||||||||||
     34 luSerAlaIleSerProAspValProAspAspCysArgValThrPheVal 50

    229 CAAGTTTTGTCTAGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAA 278
        ||||||||||||||||||||||||||||||||||||||||||||  |||||
     51 GlnValLeuSerArgHisGlyAlaArgTyrProThrSerSerLysSerLy 67

    279 GGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCA 328
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     67 sAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAlaThrAlaPheL 84

    329 AGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     84 ysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

    379 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTT 428
        ||||||||||||||||||:::|||||||||||||||||||||||||||||
    101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPh 117

    429 CTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAG 478
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    117 eTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgA 134
```

```
479 CTTCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGT 528
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
134 laSerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGly 150

529 TTCCAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTC 578
    ||||||||||||||||||||||||||||||||:::::::|||||||||||||||
151 PheGlnSerAlaLysLeuAlaAspProGlySerGlnProHisGlnAlaSe 167

579 TCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAACAACACTT 628
    ||||||||||:::|||||||||||||||||||:::|||||||||||||||||
167 rProValIleAspValIleIleProGluGlySerGlyTyrAsnAsnThrL 184

629 TGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGAC 678
    ||||||||||||   |||||||||||||||:::|||||||||||||||||||
184 euAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

679 GTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATT 728
    ||||||||||||||||||||||:::|||||||||   ||||||||||||||
201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLe 217

729 GGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACT 778
    |||||||   ||||||||||||:::|||||||||||||||||||||||   |
217 uGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrL 234

779 TGATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACT 828
    ||||||||||||||||||||:::|||||||||||||||||||||||||||||
234 euMetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThr 250

829 CAATTGTCTCCATTCTGTGACTTGTTCACTCACGACGAATGGATTCAATA 878
    :::|||||||||||||||   ||||||||||||||||||||   |||||
251 GluLeuSerProPheCysAlaLeuPheThrHisAspGluTrpArgGlnTy 267

879 CGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACC 928
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
267 rAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnP 284

929 CATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGA 978
    ||||||||||||||||||||||||||||||||:::|||||||||||||||||
284 roLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

979 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGA 1028
    ||||||:::||||||||||||||||||||||||||||||||||||||||||||
301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAs 317

1029 CTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCT 1078
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
317  pSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheS 334

1079 CTCACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAAC 1128
     ||||||||||||:::|||:::||||||||||||||||||||||||||||||||
334  erHisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsn 350

1129 GGTACTAAGCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGA 1178
     ||||||   ||||||||||||||||||||||||||||||||||||||||||
351  GlyThrAlaProLeuSerThrThrSerValGluSerIleGluGluThrAs 367

1179 CGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTG 1228
     ||||||||||||||||||||||||||||||||:::|||||||||||||||||
367  pGlyTyrSerAlaSerTrpThrValProPheGlyAlaArgAlaTyrValG 384

1229 AAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
     ||||||||||||||:::|||||||||||||||||||||||||||||||||||
384  luMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAG 1328
     ||||||||||||||||||||||||||||||||:::|||||||||||||||||
401  AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyAr 417

1329 ATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTG 1378
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
417  gCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyG 434

1379 GTAACTGGGAAGAATGTTTCGCT 1401
```

```
        ||||||||   ||||||||||||
     434 lyAsnTrpAlaGluCysPheAla 441

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-2

seq_documentation_block:
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2


alignment_scores:
           Quality: 2170.00              Length:    487
             Ratio:  5.000                Gaps:      2
 Percent Similarity:  89.117   Percent Identity: 85.421

alignment_block:
 US-09-488-265-30 x US-09-121-425-2   ..

 Align seg 1/1  to: US-09-121-425-2  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      17 rSerGlyThrAlaLeuGlyProArgGlyAsnSerHisSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      34 alAspGlyGlyTyrGlnCysPheProGluIleSerHisLeuTrpGlyGln 50

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         |||||||||:::|||||||||   ||||||||||||||||||||||||||
      51 TyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAspVa 67

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||      ||||||||||||||||||||||||||||||||||||||||||
      67 lProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||||||   ||||||||||||||||||
      84 laArgTyrProThrSerSerLysSerLysAlaTyrSerAla..... 97

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      97 ..................................................  97

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||:
      98 .ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluA 114

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ::|||||||||||||||||||||||||||||||||||||||||||||||||
     114 snGlnMetValAsnSerGlyIleLysPheTyrArgArgTyrLysAlaLeu 130
```

```
 451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 131 AlaArgLysIleValProPheIleArgAlaSerGlySerAspArgValIl 147

 501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 147 eAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaA 164

 551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC..... 591
     ||||||||::::::||||||||||||||||||||||||:::
 164 spProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

 591 ..................................................... 591

 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLy 197

 592 .GTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTT 640
      ||||||||||||||||||:::||||||||||||||||||||||||||||
 197 sValIleIleProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyT 214

 641 TGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAAC 690
       ||||||||||||||||:::||||||||||||||||||||||||||||||
 214 hrCysThrAlaPheGluAspSerGluLeuGlyAspAspValGluAlaAsn 230

 691 TTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTT 740
     |||||||||:::|||||||||   ||||||||||||||||||||   ||
 231 PheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAspLe 247

 741 GCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGT 790
     ||||||||||:::||||||||||||||||||||   ||||||||||||||
 247 uProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetC 264

 791 GTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
     ||||||||:::|||||||||||||||||||||||||||:::|||||||||
 264 ysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

 841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCA 890
     ||||||   ||||||||||||||||||||   ||||||||||||||||||
 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGl 297

 891 ATCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAG 940
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 297 nSerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProA 314

 941 CTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCT 990
     ||||||||||||||||||:::||||||||||||||||||||||:::|||
 314 laGlnGlyValGlyPheAlaAsnGluLeuIleAlaArgLeuThrArgSer 330

 991 CCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGC 1040
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 331 ProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnProAl 347

1041 TACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACA 1090
     ||||||||||||||||||||||||||||||||||||||||||||||||:
 347 aThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnS 364

1091 CTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
     ::|||:::|||||||||||||||||||||||||||||||||   |||
 364 erMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGC 1190
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAl 397

1191 TTCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAAT 1240
     ||||||||||||||||||:::|||||||||||||||||||||||||||||
 397 aSerTrpThrValProPheGlyAlaArgAlaTyrValGluMetMetGlnC 414

1241 GTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTT 1290
     ||:::||||||||||||||||||||||||||||||||||||||||||||
 414 ysGlnAlaGluLysGluProLeuValArgValLeuValAsnAspArgVal 430
```

```
1291 GTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGA 1340
     ||||||||||||||||||:::|||||||||||||||||||||||||||||
 431 ValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArgAs 447

1341 CGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAG 1390
     ||||||||||||||||||||||||||||||||||||||||||||||||  |
 447 pAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaG 464

1391 AATGTTTCGCT 1401
     |||||||||||
 464 luCysPheAla 467
```

```
seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-33

seq_documentation_block:
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
```

```
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33


alignment_scores:
           Quality: 1888.00              Length:    467
             Ratio:  4.506                Gaps:      2
 Percent Similarity:  89.722   Percent Identity: 76.874

alignment_block:
 US-09-488-265-30 x US-08-868-435-33   ..

 Align seg 1/1  to: US-08-868-435-33  from: 1  to: 465

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||   :::::::::   |||||||||   |||   |||::::::::::
       1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
           ::::::|||   :::      |||  |||   ||||||||||||
      17 gValSerAlaAlaProSerSerAlaGly...SerLysSerCysAspThrV 33

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||   |||      ||||||||||||||||
      33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         ||||||||||||||||||||   ||||||   :::::::|||      ::
      50 TyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLe 66

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         :|||||||   |||||||:::|||:::|||||||||||||||||||||||||
      66 uProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyA 83

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||||||||   ||||||   |||:::   |||:::
      83 laArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         |||||||||   |||||||||   ||||||||||||:::||||||||||||
     100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLy 116

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     116 sThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluG 133

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         |||||:::|||||||||||||||||||||||:::|||||||||||||||
     133 lnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeu 149

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         ||||||:::::|||||||||||||||||||||||||||||||||||||||
     150 AlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIl 166

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::|||||||||||||||||||||||||:::|||||||||||||
     166 eAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaA 183

     551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
         ||||||||||||:::   ::::::|||:::|||:::|||:::|||||||||
     183 spProGlyAlaThr...AsnArgAlaAlaProAlaIleSerValIleIle 198

     601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
         |||||||:::      :::||||||||||||||||||||||:::||||||
     199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLy 215

     651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
          ||||||   |||:::||||||||:::|||   |||||||||||||||:
     215 sPheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaL 232

     701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
         ::|||||||||   ||||||||||||   |||   ||||||||||||||||
     232 euPheAlaProAspIleArgAlaArgAlaGluLysHisLeuProGlyVal 248

     751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
         :::|||||||||||||||||||||||:::||||||||||||||||   |||||
     249 ThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAs 265

     801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
         ||||||||||||||||||||||||||:::|||||||||||||||||||:::|
     265 pThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnL 282

     851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
         ||||||||||||:::||||||   :::|||:::|||||||||||||||||||
     282 euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||||||||||||||||||||||||||||||||||||||::
     299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl 315

     951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         :|||||||:::|||||||||||||||||||||||||:::||||||||||||
     315 eGlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnA 332

    1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
         ||||||||||||||||   ||||||   ||||||||||||||||||||||
     332 spHisThrSerThrAsnSerThrLeuValSerAsnProAlaThrPhePro 348

    1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
         ||||||||||||:::|||:::||||||||||||||||||:::|||||||||
     349 LeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSe 365

    1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
         ||||||||||||||||||||||||||||||||:::|||||||||   |
     365 rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382

    1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
         ||||||||||||||   :::|||   |||||||||||||||||||:::
     382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

    1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
         |||||||||:::||||||||||||   |||   |||||||||:::::||
     399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGl 415

    1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
         ||||||||||||||||||:::|||:::||||||||||||||||||||||||
     415 uLysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuH 432

    1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
         ||||||||   |||||||||||||||||||||||   :::|||||||||
     432 isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448

    1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
         :::|||||||||:::|||||||||||||||||||||   ||||||||::
     449 LysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSe 465

    1401 T 1401
         :
     465 r 465

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-33

seq_documentation_block:
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
```

```
;       STREET:  340 Kingsland Street
;       CITY:  Nutley
;       STATE:  New Jersey
;       COUNTRY:  United States of America
;       ZIP:  07110
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/744,231
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/424,757
;       FILING DATE:  18-APR-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kass, Alan P
;       REGISTRATION NUMBER:  32142
;       REFERENCE/DOCKET NUMBER:  Case Docket 9339
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (201) 235-4205
;       TELEFAX:  (201) 235-2363
;   INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  465 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  104
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  119
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  205
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  228
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  337
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  374
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33


alignment_scores:
            Quality: 1888.00              Length:    467
              Ratio:  4.506                Gaps:      2
 Percent Similarity:  89.722   Percent Identity: 76.874

alignment_block:
 US-09-488-265-30 x US-08-744-231-33   ..

 Align seg 1/1  to: US-08-744-231-33  from: 1  to: 465

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||   :::::::::   |||||||||   |||   |||::::::::::
       1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
            ::::::|||   :::      |||   |||   ||||||||||||||

      17 gValSerAlaAlaProSerSerAlaGly...SerLysSerCysAspThrV 33

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||   |||       ||||||||||||||||
      33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         ||||||||||||||||||||   ||||||   ::::::|||      ::
      50 TyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLe 66

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         :||||||   ||||||:::|||:::|||||||||||||||||||||||||
      66 uProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyA 83

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||||||||   ||||||   |||:::   |||:::
      83 laArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         |||||||||   |||||||||   ||||||||||||:::||||||||||
     100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLy 116

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     116 sThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluG 133

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         |||||:::||||||||||||||||||||||||:::||||||||||||||||
     133 lnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeu 149

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         ||||||:::::|||||||||||||||||||||||||||||||||||||||
     150 AlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIl 166

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::|||||||||||||||||||||||||:::||||||||||||
     166 eAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaA 183

     551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
         ||||||||||||:::   ::::::|||:::|||:::|||:::||||||||||
     183 spProGlyAlaThr...AsnArgAlaAlaProAlaIleSerValIleIle 198

     601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
         ||||||:::      :::|||||||||||||||||||||:::||||||
     199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLy 215

     651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
          ||||||   |||:::||||||||||:::|||   |||||||||||||||:
     215 sPheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaL 232

     701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
         ::|||||||||   ||||||||||||   |||   ||||||||||||||||
     232 euPheAlaProAspIleArgAlaArgAlaGluLysHisLeuProGlyVal 248

     751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
         :::|||||||||||||||||||||:::|||||||||||||||||   |||||
     249 ThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAs 265

     801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
         ||||||||||||||||||||||||||:::|||||||||||||||||||:::|
     265 pThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnL 282

     851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
         ||||||||||:::||||||   :::|||:::||||||||||||||||||
     282 euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||||||||||||||||||||||||||||||||||||||::
     299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl 315

     951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         :|||||||:::||||||||||||||||||||||||:::||||||||||||||
     315 eGlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnA 332
```

```
1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||||||||||||||||   ||||||   ||||||||||||||||||||
 332 spHisThrSerThrAsnSerThrLeuValSerAsnProAlaThrPhePro 348

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
     ||||||||||||:::|||:::|||||||||||||||||||:::||||||||
 349 LeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSe 365

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
     ||||||||||||||||||||||||||||||||:::|||||||||   |
 365 rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||||||||||||   :::|||   ||||||||||||||||||:::
 382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
     |||||||||:::|||||||||||   |||   |||||||||:::::||
 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGl 415

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     ||||||||||||||||||:::|||:::|||||||||||||||||||||||
 415 uLysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuH 432

1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||   ||||||||||||||||||||   :::|||||||||
 432 isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
     :::|||||||||:::|||||||||||||||||||||   |||||||||::
 449 LysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSe 465

1401 T 1401
     :
 465 r 465
```

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-923-724-8

seq_documentation_block:

```
; Sequence 8, Application US/07923724
; Patent No. 5780292
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,724
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  1050.0240004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-923-724-8
```

alignment_scores:

```
            Quality: 1852.00              Length:    467
              Ratio:  4.452                Gaps:      0
 Percent Similarity:  89.079   Percent Identity: 74.304
```

alignment_block:

US-09-488-265-30 x US-07-923-724-8 ..

Align seg 1/1 to: US-07-923-724-8 from: 1 to: 467

```
   1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
     ||||||||   :::|||||||||   :::      |||   |||   ||
   1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

  51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
     |||||||   |||:::          |||:::   :::||||||||||
  17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

 101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
     |||||   ||||||||||||||||   |||   ||||||||||||||||
  34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

 151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
     |||:::|||||||||||||||||:::|||||||||||||||||||||||
  51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

 201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
     ||||   |||||||||||||||||:::|||||||||||||||||||||||
  67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

 251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
     ||||||||||||||:::|||   :::|||   ||||||||||||||||||
  84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

 301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
        ||||||:::|||:::|||:::|||   ||||||||||||||||||||
 101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

 351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
     ||||||||||||:::|||||||||||||||||||||||||||||||||||
 117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

 401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
     ||:::::|||||||||||||||||||||||:::||||||:::::|||||
 134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

 451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
     :::|||:::|||:::|||||||||||:::|||||||||:::||||||||
 151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167
```

```
 501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
     |||||||:::|||||||||||||||||||||||||||||:::||||||   |
 167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

 551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
     |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
        |||:::::::::   ||||||||||||||||   |||   |||||||::
 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
     :||||||:::|||||||||:::|||   ||||||||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

 701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
     ::|||||||||   ||||||   |||||||||      |||   ||||||
 234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
     :::||||||||||   :::|||:::   |||||||||||||||   |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
     ||||:::::::   ::::::      |||:::|||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
     |||||||||||||||||||||:::|||||||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
     ||||||||||||:::|||||||||||||||||||||||||:::|||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
     ||||:::::::|||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   |||||||:::|||||||||||||||||||||||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
     ||||||:::|||||||||||||||||||||||||||||   ::::::||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||:::|||||:::|||   :::|||||||||:::|||:::::::||||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
     ||||||||||||:::|||   |||||||||||||||||||:::|||||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     |:::|||||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||   :::|||   ||||||||||||   ||||||:::|||||||
 434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
     :::|||||||||||||||||||||||||:::|||   ||||||   ||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

1401 T 1401
```

```
      |
     467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-8

seq_documentation_block:
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    APPLICANT:  Houston, Christine S.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,426A
;      FILING DATE:  01-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/923,724
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reed, Grant E.
;      REGISTRATION NUMBER:  P-41,264
;      REFERENCE/DOCKET NUMBER:  1050.008000I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-609-426A-8


alignment_scores:
           Quality: 1852.00                Length:    467
             Ratio:  4.452                   Gaps:      0
 Percent Similarity:  89.079   Percent Identity: 74.304

alignment_block:
 US-09-488-265-30 x US-08-609-426A-8    ..
```

```
Align seg 1/1  to: US-08-609-426A-8  from: 1  to: 467

      1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
        |||||||||   :::||||||||||   :::      |||   |||   ||
      1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

     51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
        |||||||   |||:::            |||:::   :::||||||||||
     17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

    101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
        |||||   ||||||||||||||   |||   ||||||||||||||||
     34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

    151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
        |||:::|||||||||||||||||:::|||||||||||||||||||||||
     51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

    201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
        ||||   ||||||||||||||||||:::|||||||||||||||||||||
     67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

    251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
        ||||||||||||||:::|||   :::|||   ||||||||||||||||||
     84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

    301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
           ||||||:::|||:::|||:::|||   ||||||||||||||||||||
    101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

    351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
        ||||||||||||:::|||||||||||||||||||||||||||||||||||
    117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

    401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
        ||:::::|||||||||||||||||||||||::|||||:::::|||
    134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

    451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
        :::|||:::|||:::|||||||||||||:::|||||||||:::|||||||
    151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167

    501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
        |||||||:::|||||||||||||||||||||||||||:::||||||   |
    167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

    551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
        |||||   |||:::|||   |||:::|||||   |||:::|||:::|||
    184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

    601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
           |||:::::::::   |||||||||||||||   |||   ||||||::
    201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

    651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
        :|||||:::|||||||||:::|||   |||||||||||||||||||||:
    217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

    701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
        ::|||||||||   ||||||   |||||||||      |||   ||||||
    234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

    751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
        :::|||||||||   :::|||:::   ||||||||||||||   |||||
    251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

    801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
        ||||:::::::   ::::::      |||:::||||||||||||||||||
    267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

    851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
        |||||||||||||||||||||||:::|||||||||||||||||||||||

    284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

    901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
        ||||||||||||:::|||||||||||||||||||||||||:::|||||||
    301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

    951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
        ||||:::::::|||||||||||||||||||||||||||||||||||:::|
    317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

   1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
        ||   ||||||:::|||||||||||||||||||||||||||||||||||
    334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

   1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
        ||||||:::|||||||||||||||||||||||||||||   ::::::||
    351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

   1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
        ||||:::|||||||||||||||||||||||||||||||||||||||||||
    367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

   1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
        ||:::|||||||:::|||   :::|||||||||:::|||:::::::|||||
    384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

   1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
        ||||||||||||:::|||   |||||||||||||||||||||:::|||||
    401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

   1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
        |:::||||||||||||||||||||||||||||||||||||||||||||||
    417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

   1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
        ||||||||   :::|||   ||||||||||||   ||||||:::||||||
    434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
        :::||||||||||||||||||||||||||||:::|||   ||||||   ||
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

   1401 T 1401
        |
    467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2

seq_documentation_block:
; Sequence 2, Application US/08374652C
; Patent No. 5834286
;  GENERAL INFORMATION:
;    APPLICANT:  NEVALAINEN, HELENA K.M.
;    APPLICANT:  PALOHEIMO, MARJA T.
;    APPLICANT:  FAGERSTROM, RICHARD B.
;    APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;    APPLICANT:  TURUNEN, MARJA K.
;    APPLICANT:  RAMBOSEK, JOHN A.
;    APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;    APPLICANT:  HOUSTON, CHRISTINE S.
;    APPLICANT:  CANTRELL, MICHAEL A.
;    TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;    TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;    TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/374,652C
;       FILING DATE:  24-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/07058
;       FILING DATE:  27-JUL-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/925,401
;       FILING DATE:  31-JUL-1992
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  REED, GRANT E.
;       REGISTRATION NUMBER:  41,264
;       REFERENCE/DOCKET NUMBER:  1050.071001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  protein
US-08-374-652C-2


alignment_scores:
            Quality: 1852.00              Length:    467
              Ratio:  4.452                Gaps:      0
 Percent Similarity:  89.079   Percent Identity: 74.304

alignment_block:
 US-09-488-265-30 x US-08-374-652C-2   ..

 Align seg 1/1  to: US-08-374-652C-2  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::     |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         |||||||   |||:::            |||:::   :::||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||||||||||||||||:::|||||||||||||||||||||||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||   |||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
            ||||||:::|||:::|||:::|||   ||||||||||||||||||||
     101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||||:::|||||||||||||||||||||||||||||||||

     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ||:::::::|||||||||||||||||||||||||||:::|||||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||:::|||||||||||||:::||||||||||:::|||||||
     151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::|||||||||||||||||||||||||||||:::|||||||
     167 eAlaSerGlyGluLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
            |||::::::::::   ||||||||||||||   |||   ||||||:
     201 SerGluAlaSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
         :||||||:::||||||||:::|||   ||||||||||||||||||||:
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
         ::|||||||||   ||||||   |||||||||      |||   ||||||
     234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
         :::||||||||||   :::|||:::   |||||||||||||||   |||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
         ||||::::::   ::::::      |||:::||||||||||||||||||
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
         |||||||||||||||||||||||:::|||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||:::|||||||||||||||||||||||||:::|||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         ||||::::::|||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
         ||   ||||||:::|||||||||||||||||||||||||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

    1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
         ||||||:::|||||||||||||||||||||||||||||   ::::::||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
         ||||:::|||||||||||||||||||||||||||||||||||||||||||
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
         ||:::|||||||:::|||   :::|||||||||:::|||:::::|||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

    1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
         ||||||||||||:::|||   |||||||||||||||||||||:::|||||
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
         |:::|||||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
```

```
   1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
        ||||||||   :::|||   ||||||||||||   ||||||:::||||||
    434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
        :::|||||||||||||||||||||||||||:::|||   ||||||   ||
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467

   1401 T 1401
        |
    467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-151-574-32

seq_documentation_block:

```
; Sequence 32, Application US/08151574
; Patent No. 5436156
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,574
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-151-574-32
```

alignment_scores:

```
            Quality: 1848.00              Length:    467
              Ratio:  4.432                Gaps:      0
 Percent Similarity:  89.293   Percent Identity: 74.304
```

alignment_block:

```
 US-09-488-265-30 x US-08-151-574-32   ..

 Align seg 1/1  to: US-08-151-574-32  from: 1  to: 467
```

```
    1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
      |||||||||   :::||||||||||   :::      |||   |||   ||
    1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

   51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
      |||||||   |||:::             |||:::   ||||||||||||||
   17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

  101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
      |||||   ||||||||||||||   |||   ||||||||||||||
   34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

  151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
      |||:::||||||||||||||||||||:::|||||||:::||||||||:::||
   51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

  201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
      ||||   ||||||||||||||||||:::|||||||||||||||||||||||
   67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

  251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
      ||||||||||||||:::|||   :::|||   ||||||||||||||||||
   84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

  301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         ||||||:::||||||||||:::|||   ||||||||||||||||||||
  101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

  351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
      ||||||||||||:::|||||||||||||||||||||||||||||||||||
  117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

  401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
      ||:::::::|||||||||||||||||||||||:::|||||||::::::|||
  134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

  451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
      :::|||:::|||||||||||||||||:::|||||||||:::|||||||||
  151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

  501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
      |||||||::::::|||||||||||||||||||||||||:::||||||   |
  167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

  551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
      |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
  184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

  601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
         |||::::::::::   ||||||||||||||   |||   ||||||:
  201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

  651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
      :||||||:::|||||||||:::|||   ||||||||||||||||||||:
  217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

  701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
      ::|||:::|||   ||||||   |||||||||      |||   ||||||
  234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

  751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
      :::|||||||||   :::|||:::   ||||||||||||||   |||||
  251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

  801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
      ||||:::::::   ::::::      |||:::||||||||||||||||||
  267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

  851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
      |||||||||||||||||||||||:::|||||||||||||||||||||||
  284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

  901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
```

```
      |||||||||||:::|||||||||||||||||||||||||:::||||||||
  301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

  951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
      ||||:::::|||||||||||||||||||||||||||||||||||||:::|
  317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

 1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
      ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
  334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

 1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
      ||||||:::|||||||||||||||||||||||||||||   :::::::||
  351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

 1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
      ||||:::|||||||||||||||||||||||||||||||||||||||||||
  367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

 1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
      ||:::|||||||:::|||   :::|||||||||:::|||:::::||||||
  384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

 1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
      ||||||||||||:::|||   |||||||||||||||||||:::|||||
  401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

 1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
      |:::||||||||||||||||||||||||||||||||||||||||||||||
  417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

 1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
      ||||||||   ||||||   ||||||||||||   |||||||::||||||
  434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

 1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
      :::|||||||||||||||||||||||||||:::|||   ||||||||||
  451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

 1401 T 1401
      |
  467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-146-424-20

seq_documentation_block:
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20


alignment_scores:
            Quality: 1848.00              Length:    467
              Ratio:  4.432                Gaps:      0
 Percent Similarity:  89.293   Percent Identity: 74.304

alignment_block:
 US-09-488-265-30 x US-08-146-424-20   ..

 Align seg 1/1  to: US-08-146-424-20  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         |||||||   |||:::           |||:::   ||||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||||||||||||||||:::|||||||:::|||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||   |||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         |||||||:::||||||||:::|||   ||||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||:::|||||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ||:::::|||||||||||||||||||||||:::|||||:::::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::|||||||||:::|||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::::|||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
```

```
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
       |||::::::::   ||||||||||||||   |||   ||||||::
 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
     :|||||:::|||||||||:::|||   ||||||||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

 701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
     ::|||:::|||   ||||||   |||||||||      |||   ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
     :::|||||||||   :::|||:::   ||||||||||||||   |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
     ||||::::::   ::::::      |||:::||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
     ||||||||||||||||||||:::|||||||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
     ||||||||||||:::|||||||||||||||||||||||||:::|||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
     ||||:::::::|||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   ||||||:::|||||||||||||||||:::|||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
     ||||||:::|||||||||||||||||||||||||||   :::::::||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||:::||||||:::|||   :::|||||||||:::|||:::::::||||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
     ||||||||||||:::|||   |||||||||||||||||||:::|||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     |:::||||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||   ||||||   ||||||||||||   ||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
     :::|||||||||||||||||||||||||||:::|||   ||||||||||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

1401 T 1401
     |  .
 467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-693-709-2

seq_documentation_block:

; Sequence 2, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
;   APPLICANT: VAN OOIJEN, ALBERT J.J.
;   APPLICANT: RIETVELD, KRIJN
;   APPLICANT: HOEKEMA, ANDREAS
;   APPLICANT: PEN, JAN
;   APPLICANT: SIJMONS, PETER C.
;   APPLICANT: VERWOERD, TEUNIS C.
;   TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
;   TITLE OF INVENTION: IN PLANTS
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: MORRISON & FOERSTER
;     STREET: 755 PAGE MILL ROAD
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/693,709
;     FILING DATE: 07-AUG-1996
;     CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/146,424
;     FILING DATE: 02-NOV-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Murashige, Kate H
;     REGISTRATION NUMBER: 29,959
;     REFERENCE/DOCKET NUMBER: 24615-20011.10
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-813-5600
;     TELEFAX: 415-494-0792
;     TELEX: 706141
;  INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 467 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FRAGMENT TYPE: internal
;   FEATURE:
;     NAME/KEY: Signal Sequence
;     LOCATION: 1...23
;     OTHER INFORMATION:
US-08-693-709-2


alignment_scores:
            Quality: 1848.00              Length:    467
              Ratio: 4.432                  Gaps:      0
 Percent Similarity: 89.293   Percent Identity: 74.304

alignment_block:
 US-09-488-265-30 x US-08-693-709-2   ..

 Align seg 1/1  to: US-08-693-709-2  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         |||||||   |||:::              |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
```

```
 34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
 51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
 67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
 84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
```

```
 334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

1401 T 1401
     |
 467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-419-448-32

```
seq_documentation_block:
; Sequence 32, Application US/08419448
; Patent No. 5863533
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-419-448-32


alignment_scores:
            Quality: 1848.00              Length:    467
              Ratio:  4.432                Gaps:      0
 Percent Similarity:  89.293   Percent Identity: 74.304

alignment_block:
 US-09-488-265-30 x US-08-419-448-32   ..

 Align seg 1/1  to: US-08-419-448-32  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::||||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         |||||||   |||:::           |||:::   ||||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||||||||||||||||||:::||||||:::|||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||   |||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         ||||||:::|||||||||:::|||   ||||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||:::||||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ||:::::|||||||||||||||||||||||||:::||||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::||||||||||:::||||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::::|||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
         |||:::::::::   ||||||||||||||   |||   |||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
         :||||||:::|||||||||:::|||   ||||||||||||||||||||:
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
         ::|||:::|||   ||||||   |||||||||      |||   ||||||
     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
         :::|||||||||   :::|||:::   ||||||||||||||   |||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
         ||||::::::   ::::::      |||:::|||||||||||||||||||
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
         |||||||||||||||||||||:::|||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||:::|||||||||||||||||||||||||:::||||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         ||||:::::|||||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
         ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

    1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
         ||||||:::|||||||||||||||||||||||||||||||   ::::::||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
         ||||:::|||||||||||||||||||||||||||||||||||||||:::|
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
         ||:::|||||:::|||   :::|||||||||:::|||:::::|||||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

    1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
         ||||||||||||:::|||   |||||||||||||||||||||:::|||||
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
         |:::|||||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

    1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
         ||||||||   ||||||   ||||||||||||   ||||||:::||||||
     434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

    1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
         :::|||||||||||||||||||||||||||:::|||   ||||||||||
     451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

    1401 T 1401
         |
     467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-3

seq_documentation_block:
; Sequence 3, Application US/08819825
; Patent No. 5866118
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-825-3


alignment_scores:
            Quality: 1848.00              Length:    467
              Ratio:  4.432                Gaps:      0
 Percent Similarity:  89.293   Percent Identity: 74.304

alignment_block:
 US-09-488-265-30 x US-08-819-825-3   ..

 Align seg 1/1  to: US-08-819-825-3  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::||||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         |||||||   |||:::            |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||||||||||||||||||:::|||||||:::||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||   |||||||||||||||||:::|||||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         ||||||:::|||||||||:::|||   ||||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||:::|||||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ||:::::|||||||||||||||||||||||:::|||||::::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::|||||||||:::||||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::::|||||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
         |||||   |||:::|||   |||:::|||||||   |||:::|||:::|||
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
            |||:::::::::   |||||||||||||||   |||   ||||||::
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
         :||||||:::||||||||:::|||   ||||||||||||||||||||:
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
         ::|||:::|||   ||||||   ||||||||      |||   ||||||
     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
         :::|||||||||   :::|||:::   ||||||||||||||   ||||
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
         ||||::::::   ::::::      |||:::||||||||||||||||||
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
         ||||||||||||||||||||||:::|||||||||||||||||||||||
     284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||:::|||||||||||||||||||||||||:::|||||||
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
         ||||:::::|||||||||||||||||||||||||||||||||||||:::|
     317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

    1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
         ||   ||||||:::|||||||||||||||||||:::|||||||||||||
     334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

    1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
         ||||||:::|||||||||||||||||||||||||||||||   :::::::||
     351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

    1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
         ||||:::|||||||||||||||||||||||||||||||||||||||||||
     367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

    1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
         ||:::||||||:::|||   :::|||||||||:::|||:::::||||||
     384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

    1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
         ||||||||||||::|||   |||||||||||||||||||:::||||||
     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

    1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
         |:::|||||||||||||||||||||||||||||||||||||||||||||
     417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
```

```
   1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
        ||||||||   ||||||   ||||||||||||   ||||||:::|||||| 
    434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

   1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
        :::|||||||||||||||||||||||||||:::|||   ||||||||||| 
    451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

   1401 T 1401
        | 
    467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-163-642-3

```
seq_documentation_block:
; Sequence 3, Application US/09163642
; Patent No. 6221644
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,642
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-163-642-3


alignment_scores:
            Quality: 1848.00              Length:    467
              Ratio:  4.432                Gaps:      0
 Percent Similarity:  89.293   Percent Identity: 74.304

alignment_block:
 US-09-488-265-30 x US-09-163-642-3   ..

 Align seg 1/1  to: US-09-163-642-3  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::||||||||||   :::      |||   |||   || 
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         |||||||   |||:::            |||:::   |||||||||||||| 
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||||||   |||   |||||||||||||||| 
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||||||||||||||||||:::||||||:::||||||||||:::|| 
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||   ||||||||||||||||||:::|||||||||||||||||||||| 
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::||||   |||||||||||||||||| 
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
            ||||||:::|||||||||:::|||   |||||||||||||||||||| 
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         |||||||||||||:::|||||||||||||||||||||||||||||||||| 
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ||:::::|||||||||||||||||||||||:::||||||:::::||| 
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::||||||||||:::|||||| 
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::::|||||||||||||||||||||||||:::||||||   | 
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
         |||||   |||:::|||   |||:::|||||||   |||:::|||:::||| 
     184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

     601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
            |||:::::::::   ||||||||||||||   |||   |||||||:: 
     201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

     651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
         :|||||:::|||||||||:::|||   |||||||||||||||||||||: 
     217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

     701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
         ::|||:::|||   ||||||   |||||||||      |||   |||||| 
     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

     751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
         :::|||||||||   :::|||:::   |||||||||||||||   ||||| 
     251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

     801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
         ||||::::::   ::::::      |||:::|||||||||||||||||| 
     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

     851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
         |||||||||||||||||||||||:::|||||||||||||||||||||| 
     284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

     901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
         ||||||||||||:::|||||||||||||||||||||||||:::|||||||| 
     301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

     951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
```

```
      |||||::::::|||||||||||||||||||||||||||||||||||||:::|
  317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

 1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
      ||   ||||||:::|||||||||||||||||||:::|||||||||||||||
  334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

 1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
      ||||||:::|||||||||||||||||||||||||||||   ::::::||
  351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

 1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
      ||||:::|||||||||||||||||||||||||||||||||||||||||||
  367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

 1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
      ||:::||||||:::|||   :::||||||||||:::|||::::::|||||
  384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

 1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
      ||||||||||||:::|||   |||||||||||||||||||||:::|||||
  401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

 1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
      |:::||||||||||||||||||||||||||||||||||||||||||||||
  417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

 1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
      ||||||||   ||||||   ||||||||||||   |||||||:::||||||
  434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

 1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
      :::|||||||||||||||||||||||||:::|||   ||||||||||||
  451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

 1401 T 1401
      |
  467 a 467
```

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-233-510-32

```
seq_documentation_block:
; Sequence 32, Application US/09233510
; Patent No. 6350602
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/233,510
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-233-510-32


alignment_scores:
            Quality: 1848.00              Length:    467
              Ratio:  4.432                Gaps:      0
 Percent Similarity:  89.293   Percent Identity: 74.304

alignment_block:
 US-09-488-265-30 x US-09-233-510-32   ..

 Align seg 1/1  to: US-09-233-510-32  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         |||||||   |||:::              |||:::   ||||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::|||||||||||||||||||:::|||||||:::||||||||||:::||
      51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||   ||||||||||||||||||:::|||||||||||||||||||||
      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
            ||||||:::|||||||||:::|||   ||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||:::||||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ||:::::|||||||||||||||||||||:::|||||||:::::|||
     134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::|||||||||:::||||||||
     151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
         |||||||:::::|||||||||||||||||||||||||:::||||||   |
     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

     551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
         |||||   |||:::|||   |||:::||||||   |||:::|||:::|||
```

```
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
       |||:::::::::   |||||||||||||||   |||   ||||||::
 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
     :|||||||:::|||||||||:::|||   ||||||||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234

 701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
     ::|||:::|||   ||||||   |||||||||       |||   ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
     :::||||||||||   :::|||:::   ||||||||||||||   |||||
 251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
     ||||::::::   ::::::      |||:::|||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
     ||||||||||||||||||||||:::|||||||||||||||||||||||||
 284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
     |||||||||||:::|||||||||||||||||||||||||:::|||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
     ||||:::::|||||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   ||||||:::|||||||||||||||||:::|||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
     ||||||:::|||||||||||||||||||||||||||||   ::::::|||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||:::|||||||:::|||   :::|||||||||:::|||:::::|||||
 384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
     ||||||||||||:::|||   |||||||||||||||||||:::||||||
 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     |:::||||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||   ||||||   ||||||||||||   ||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
     :::|||||||||||||||||||||||||:::|||   ||||||||||||
 451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467

1401 T 1401
     |
 467 a 467

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-3

seq_documentation_block:
```

```
; Sequence 3, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
;  APPLICANT: KONDO, Hidemasa
;  APPLICANT: ANAZAWA, Hideharu
;  APPLICANT: KANEKO, Syunichi
;  APPLICANT: NAGASHIMA, Tadashi
;  APPLICANT: TANGE, Tatsuya
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 81356/124
;  CURRENT APPLICATION NUMBER: US/09/155,855
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
;  EARLIER FILING DATE: 1997-04-04
;  EARLIER APPLICATION NUMBER: JP 084314
;  EARLIER FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-155-855-3


alignment_scores:
           Quality: 1841.00              Length:    467
             Ratio:  4.394                Gaps:      0
 Percent Similarity:  89.722   Percent Identity: 73.233

alignment_block:
 US-09-488-265-30 x US-09-155-855-3   ..

 Align seg 1/1  to: US-09-155-855-3  from: 1  to: 467

       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
         |||||||||   :::|||||||||   :::      |||   |||   ||
       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17

      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
         |||||||   |||:::             |||:::   :::||||||||||
      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34

     101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
         |||||   ||||||||||||||   |||   ||||||||||||||||
      34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50

     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
         |||:::||||||||||||||||||:::::|||||||||||||||||||||
      51 TyrAlaProPhePheSerLeuAlaAsnLysSerAlaIleSerProAspVa 67

     201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
         ||||   ||||||:::|||||||||:::|||||||||||||||||||||
      67 lProAlaGlyCysHisValThrPheAlaGlnValLeuSerArgHisGlyA 84

     251 CTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
         ||||||||||||||:::|||   :::|||   ||||||||||||||||||
      84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
         ||||||:::|||||||||:::|||:::|||||||||||||||||||||||
     101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLy 117

     351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
         ||||||||||||:::|||||||||||||||||||||||||||||||||||
     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134

     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
         ||:::::::|||||||||||:::|||||||:::|||||::::::|||||
     134 lnGluLeuValAsnSerGlyValLysPheTyrGlnArgTyrGluSerLeu 150

     451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
         :::|||:::|||||||||||||||||||:::|||||||||:::||||||||
```

```
 151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167

 501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
     |||||||:::::|||||||||||||||||||||||||||:::|||||| |
 167 eAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184

 551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
     |||||   |||:::|||  |||:::|||||  |||:::|||:::|||
 184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

 601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
       |||::::::      ||||||||||||||  |||   ||||||::
 201 SerGluAlaSerThrSerAsnAsnThrLeuAspProGlyThrCysThrVa 217

 651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
     :|||||||:::|||||||||:::|||||||:::|||||||||||||||:
 217 lPheGluAspSerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaT 234

 701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
     ::|||:::|||  ||||||  ||||||||      |||  ||||||
 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250

 751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
     :::|||||||||  :::|||:::  |||||||||||||||  |||||
 251 SerLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267

 801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
     ||||::::::  ::::::      |||:::||||||||||||||||||
 267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284

 851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
     |||||||||||:::|||||||||:::|||||||||||||||||||||:::
 284 euPheThrHisGluGluTrpIleAsnTyrAspTyrLeuGlnSerLeuAsn 300

 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
     ||||||||||||:::|||||||||||||||||||||||||:::||||||||
 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317

 951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
     ||||:::::|||||||||||||||||||||||||||||||||||||:::|
 317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334

1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
     ||   ||||||:::|||||||||||||||||||||||||||||||||||
 334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350

1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
     |||||||:::|||||||||||||||||||||||||||||||  ::::::||
 351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367

1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
     ||||:::|||||||||||||||||||||||||||||||||||||||:::|
 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerSerT 384

1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
     ||::::::|||:::|||  :::|||||||||:::|||::::::||||||
 384 hrThrAlaGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
     ||||||||||||:::|||  ||||||||||||||||||||::::::||
 401 ValProPheAlaSerArgMetTyrValGluMetMetGlnCysGlnSerGl 417

1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
     |:::|||||||||||||||||||||||||||||||||||||||||||||
 417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434

1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
     ||||||||  ||||||  ||||||||||||  ||||||:::||||||
 434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450

1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
     :::|||||||||||||||||||||||||||:::|||  ||||||||||
 451 LysGlyLeuSerPheAlaArgSerGlyGlyAspTrpGlyGluCysPheAl 467
```

```
1401 T 1401
     |
 467 a 467
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 3, 2002, 09:33:14 ; Search time 39.56 Seconds
(without alignments)
288.341 Million cell updates/sec

Title: US-09-488-265-31
Perfect score: 2468
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWEECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2182	88.4	441	4	US-09-121-425-1	Sequence 1, Appli
2	2170	87.9	467	4	US-09-121-425-2	Sequence 2, Appli
3	1888	76.5	465	4	US-08-868-435-33	Sequence 33, Appl
4	1888	76.5	465	4	US-08-744-231-33	Sequence 33, Appl
5	1852	75.0	467	1	US-07-923-724-8	Sequence 8, Appli
6	1852	75.0	467	2	US-08-609-426A-8	Sequence 8, Appli
7	1852	75.0	467	2	US-08-374-652C-2	Sequence 2, Appli
8	1848	74.9	467	1	US-08-151-574-32	Sequence 32, Appl
9	1848	74.9	467	1	US-08-146-424-20	Sequence 20, Appl
10	1848	74.9	467	1	US-08-693-709-2	Sequence 2, Appli
11	1848	74.9	467	2	US-08-419-448-32	Sequence 32, Appl
12	1848	74.9	467	2	US-08-819-825-3	Sequence 3, Appli
13	1848	74.9	467	4	US-09-163-642-3	Sequence 3, Appli
14	1848	74.9	467	4	US-09-233-510-32	Sequence 32, Appl
15	1841	74.6	467	4	US-09-155-855-3	Sequence 3, Appli
16	1841	74.6	467	4	US-09-543-744-3	Sequence 3, Appli
17	1822	73.8	466	4	US-08-868-435-35	Sequence 35, Appl
18	1822	73.8	466	4	US-08-744-231-35	Sequence 35, Appl
19	1819	73.7	466	4	US-08-868-435-12	Sequence 12, Appl
20	1819	73.7	466	4	US-08-744-231-12	Sequence 12, Appl
21	1804.5	73.1	463	4	US-08-868-435-29	Sequence 29, Appl
22	1804.5	73.1	463	4	US-08-744-231-29	Sequence 29, Appl
23	1799	72.9	443	4	US-09-155-855-1	Sequence 1, Appli
24	1799	72.9	443	4	US-09-543-744-1	Sequence 1, Appli
25	1794	72.7	443	4	US-09-155-855-2	Sequence 2, Appli
26	1794	72.7	443	4	US-09-543-744-2	Sequence 2, Appli
27	1752	71.0	466	4	US-08-868-435-2	Sequence 2, Appli
28	1752	71.0	466	4	US-08-744-231-2	Sequence 2, Appli
29	1710	69.3	466	4	US-08-868-435-31	Sequence 31, Appl
30	1710	69.3	466	4	US-08-744-231-31	Sequence 31, Appl
31	1381	56.0	475	2	US-08-819-825-2	Sequence 2, Appli
32	1381	56.0	475	4	US-09-163-642-2	Sequence 2, Appli
33	1334.5	54.1	487	4	US-08-868-435-4	Sequence 4, Appli
34	1334.5	54.1	487	4	US-08-744-231-4	Sequence 4, Appli
35	845.5	34.3	443	3	US-08-993-359-30	Sequence 30, Appl
36	833.5	33.8	453	3	US-08-993-359-22	Sequence 22, Appl
37	830.5	33.7	439	3	US-08-993-359-24	Sequence 24, Appl
38	830.5	33.7	439	3	US-09-221-654-2	Sequence 2, Appli
39	830.5	33.7	439	3	US-08-989-358A-2	Sequence 2, Appli
40	825	33.4	442	3	US-08-993-359-28	Sequence 28, Appl
41	814	33.0	442	3	US-08-993-359-26	Sequence 26, Appl
42	359	14.5	468	1	US-07-627-539G-2	Sequence 2, Appli
43	354.5	14.4	446	1	US-07-627-539G-7	Sequence 7, Appli
44	354.5	14.4	479	1	US-07-923-724-2	Sequence 2, Appli
45	354.5	14.4	479	2	US-08-609-426A-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

  Query Match            88.4%;  Score 2182;  DB 4;  Length 441;
  Best Local Similarity  93.0%;  Pred. No. 6.6e-217;
  Matches  410;  Conservative   11;  Mismatches   20;  Indels    0;  Gaps    0;

Qy      27 NSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 86
           ||||||||||||||||||||||| |||:||| |||||||||| ||||||||||||||||
Db       1 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 60

Qy      87 PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
           |||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      61 PTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

Qy     147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY 206
           |||||||||||||||||||||||||||||||||||||: ||||||||:||||||:||
Db     121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy     207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
           ||||||| |||||:||||||||||:||| ||||||| |||| |||||||| |||||||
Db     181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

Qy     267 DTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
           :|||||||||:||||| ||||||| |||||||||||||||||||||||||||| ||||||
Db     241 ETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300

Qy     327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
           || |||||||||||||||||||||||||||||:|:|||||||||||| |||||||
```

```
Db    301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy    387 ESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
          ||||||||||||||||| |||||||||:||||||||||||||||||| |||||||||
Db    361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy    447 DDFVEGLSFARSGGNWEECFA 467
          ||||||||||||||| ||||
Db    421 DDFVEGLSFARSGGNWAECFA 441


RESULT   2
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2


  Query Match             87.9%;  Score 2170;  DB 4;  Length 467;
  Best Local Similarity   85.4%;  Pred. No. 1.3e-215;
  Matches  416;  Conservative   11;  Mismatches   20;  Indels   40;  Gaps    2;

Qy      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||:||| ||
Db      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy     61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
          ||||||||  |||||||||||||||||||| ||||||                   |||
Db     61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSA--------------------TYN 100

Qy    121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160

Qy    181 KLADPGANPHQASPVIN--------------------VIIPEGAGYNNTLDHGLCTAFEE 220
          ||||||: ||||||||:                    ||||||:||||||||| |||||:
Db    161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy    221 SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSP 280
          |||||||||||||:||| ||||||| |||| ||||||| |||||||:||||||||:|||
Db    221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

Qy    281 FCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNH 340
          || ||||||| |||||||||||||||||||||||||| |||||||| ||||||||||||||
Db    281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy    341 TLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWT 400
          |||||||||||||||||||||||:|:|||||||||||| ||||||||||||||||||||||
Db    341 TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

Qy    401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGG 460
          ||| ||||||||||:|||||||||||||||||||| ||||||||||||||||||||||||
Db    401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460

Qy    461 NWEECFA 467
          || ||||
Db    461 NWAECFA 467


RESULT   3
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33


  Query Match             76.5%;  Score 1888;  DB 4;  Length 465;
  Best Local Similarity   76.9%;  Pred. No. 1.7e-186;
```

Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

```
Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
Db       1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db      60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db     120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db     180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db     239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db     299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db     359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db     419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
```

```
RESULT   4
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33
```

Query Match 76.5%; Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.7e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

```
Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
Db       1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db      60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db     120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db     180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db     239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db     299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db     359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db     419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
```

```
RESULT   5
US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
```

```
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,724
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  1050.0240004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-923-724-8


  Query Match             75.0%;  Score 1852;  DB 1;  Length 467;
  Best Local Similarity   74.3%;  Pred. No. 9.2e-183;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:|||||:|
Db       1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           |||||||| |||||| |||||||||||| |  | |||||| ||:| | | ||||||||||
Db      61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||::|||||||:||::| | |:||||:||| ||||| |||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | |||||||| ||| ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
```

```
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||: |||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| ||||||||||||||:||:| :|||:|::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| :| |||| || || |||||||||:| || |
Db     421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT   6
US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    APPLICANT:  Houston, Christine S.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,426A
;      FILING DATE:  01-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/923,724
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reed, Grant E.
;      REGISTRATION NUMBER:  P-41,264
;      REFERENCE/DOCKET NUMBER:  1050.0080001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-609-426A-8


  Query Match             75.0%;  Score 1852;  DB 2;  Length 467;
  Best Local Similarity   74.3%;  Pred. No. 9.2e-183;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:|||||:|
Db       1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           |||||||| |||||| |||||||||||| |  | |||||| ||:| | | ||||||||||
Db      61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||::|||||||:||:::| | |:||||:||| ||||| |||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| ||| ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||:|::|||||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| :| |||| || || |||||||||:| || |
Db     421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT   7
US-08-374-652C-2
; Sequence 2, Application US/08374652C
; Patent No. 5834286
;  GENERAL INFORMATION:
;    APPLICANT:  NEVALAINEN, HELENA K.M.
;    APPLICANT:  PALOHEIMO, MARJA T.
;    APPLICANT:  FAGERSTROM, RICHARD B.
;    APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;    APPLICANT:  TURUNEN, MARJA K.
;    APPLICANT:  RAMBOSEK, JOHN A.
;    APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;    APPLICANT:  HOUSTON, CHRISTINE S.
;    APPLICANT:  CANTRELL, MICHAEL A.
;    TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;    TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;    TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,652C
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07058
;      FILING DATE:  27-JUL-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/925,401
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REED, GRANT E.
;      REGISTRATION NUMBER:  41,264
;      REFERENCE/DOCKET NUMBER:  1050.071001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-374-652C-2


  Query Match             75.0%;  Score 1852;  DB 2;  Length 467;
  Best Local Similarity   74.3%;  Pred. No. 9.2e-183;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:|||||:|
Db       1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           |||||||| |||||| |||||||||||| |  | |||||| ||:| | | ||||||||||
Db      61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||::|||||||:||:::| | |:||||:||| ||||| |||||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| ||| ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||:|::|||||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| :| |||| || || |||||||||:| || |
Db     421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT   8
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
```

```
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,574
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-151-574-32


  Query Match           74.9%;  Score 1848;  DB 1;  Length 467;
  Best Local Similarity  74.3%;  Pred. No. 2.4e-182;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::|||||||:||::| | ||||||:||| ||||| :|||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
            |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||| |||||||||||| | ||:|||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| ||||||||||||||:||:| :|||:|:::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           ||||||||||||||| || |||| || || |||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  9
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20


  Query Match           74.9%;  Score 1848;  DB 1;  Length 467;
  Best Local Similarity  74.3%;  Pred. No. 2.4e-182;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::|||||||:||::| | ||||||:||| ||||| :|||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
            |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
```

```
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:||||||| |||||: |||||||||||| | ||:||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||:|::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || |||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 10
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J.J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/693,709
;      FILING DATE:  07-AUG-1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/146,424
;      FILING DATE:  02-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20011.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Signal Sequence
;      LOCATION:  1...23
;      OTHER INFORMATION:
US-08-693-709-2


  Query Match             74.9%;  Score 1848;  DB 1;  Length 467;
  Best Local Similarity   74.3%;  Pred. No. 2.4e-182;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:|||||||||||::|||||||:||::| | ||||||:||| ||||| :|||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
           |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:||||||| |||||: |||||||||||| | ||:||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||:|::|||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || |||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 11
US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-419-448-32

Query Match 74.9%; Score 1848; DB 2; Length 467;
Best Local Similarity 74.3%; Pred. No. 2.4e-182;
Matches 347; Conservative 42; Mismatches 78; Indels 0; Gaps 0;

```
Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467
```

RESULT 12
US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,825
; FILING DATE: 18-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-819-825-3

Query Match 74.9%; Score 1848; DB 2; Length 467;
Best Local Similarity 74.3%; Pred. No. 2.4e-182;
Matches 347; Conservative 42; Mismatches 78; Indels 0; Gaps 0;

```
Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467
```

RESULT 13
US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

```
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,642
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-163-642-3


  Query Match             74.9%;  Score 1848;  DB 4;  Length 467;
  Best Local Similarity   74.3%;  Pred. No. 2.4e-182;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::|||||||:||::| | |||||||||| |||||  :|||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
            |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||:|:::|||||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || ||||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT  14
US-09-233-510-32
; Sequence 32, Application US/09233510
; Patent No. 6350602
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/233,510
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-233-510-32


  Query Match             74.9%;  Score 1848;  DB 4;  Length 467;
  Best Local Similarity   74.3%;  Pred. No. 2.4e-182;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|||||:|
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           | |||:|| |||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::|||||||:||::| | |||||||||| |||||  :|||||||
Db     121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| | ||||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
            |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||| |||||||
Db     241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:|||||||:|||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| |||||||||||||||:||:| :|||:|:::|||||||:| |||||||:||:||
Db     361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || || ||||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467
```

```
Db    421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 15
US-09-155-855-3
; Sequence 3, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
;  APPLICANT: KONDO, Hidemasa
;  APPLICANT: ANAZAWA, Hideharu
;  APPLICANT: KANEKO, Syunichi
;  APPLICANT: NAGASHIMA, Tadashi
;  APPLICANT: TANGE, Tatsuya
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 81356/124
;  CURRENT APPLICATION NUMBER: US/09/155,855
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
;  EARLIER FILING DATE: 1997-04-04
;  EARLIER APPLICATION NUMBER: JP 084314
;  EARLIER FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-155-855-3


  Query Match             74.6%;  Score 1841;  DB 4;  Length 467;
  Best Local Similarity   73.2%;  Pred. No. 1.3e-181;
  Matches  342;  Conservative   49;  Mismatches   76;  Indels    0;  Gaps    0;

Qy       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
           |||  ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:||||||::
Db       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANK 60

Qy      61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
           |||||||| || ||| |||||||||||| |  | |||||| ||:||| |:||||||||||
Db      61 SAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFEGKYAFLKTYN 120

Qy     121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           |:||||||||||||::||||:|||:||::| | ||||||:||| ||||  ||||||||
Db     121 YSLGADDLTPFGEQELVNSGVKFYQRYESLTRNIVPFIRSSGSSRVIASGNKFIEGFQST 180

Qy     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
           || || | | |:|| |:|:| | :  ||||| | || ||:||| ||:|||||| | | ||
Db     181 KLKDPRAQPGQSSPKIDVVISEASTSNNTLDPGTCTVFEDSELADDIEANFTATFVPSIR 240

Qy     241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
            |||  | ||:||| :|  ||||| |||:: ::  |:||||||||||:||| |||||||
Db     241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHEEWINYDYLQSLN 300

Qy     301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
           ||||:|||||||| |||||: |||||||||||| | ||:||||||||||||||:|||||||
Db     301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
           ||| ::|| ||||||||||||:|: |:| :|||:|::|||||:| |||||||::|:||
Db     361 HDNGIISILFALGLYNGTKPLSSTTAENITQTDGFSSAWTVPFASRMYVEMMQCQSEQEP 420

Qy     421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
           |||||||||||||||| || |||| || ||:||||||||:| ||||
Db     421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVKGLSFARSGGDWGECFA 467


Search completed: July  3, 2002, 09:33:16
Job time: 155 sec
```